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                    GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          August 13, 2004, 19:06:21 ; Search time 516 Seconds
                                              (without alignments)
                                              5258.438 Million cell updates/sec

Title:           US-10-044-205A-2
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Searched:        3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters:      6451454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
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Database :       Published_Applications_NA:*
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES
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    2    2889  100.0   2198  14  US-10-044-205A-1        Sequence 1, Appli
    3    2883   99.8   1662  15  US-10-217-745-1         Sequence 1, Appli
    4    2883   99.8   1662  17  US-10-311-034-45        Sequence 45, Appl
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    6    2883   99.8   2249  15  US-10-217-745-5         Sequence 5, Appli
    7    2876   99.6   1662   9  US-09-964-469-1        Sequence 1, Appli
    8    2876   99.6   1662  15  US-10-425-962-1         Sequence 1, Appli
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                              ALIGNMENTS

RESULT 1
US-10-044-205A-3
; Sequence 3, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
;  APPLICANT: KAPELLER-LIBERMANN, Rosana
;  APPLICANT:  BANDARU, Rajasekhar
;  TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Proteir
;  TITLE OF INVENTION:  Uses Thereof
;  FILE REFERENCE: 10147-52U1
;  CURRENT APPLICATION NUMBER: US/10/044,205A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: US 60/242,428
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: US 60/241,884
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 60/241,877
;  PRIOR FILING DATE: 2000-10-20
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 1659
;   TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-044-205A-3

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Score:                    2889.00       Matches:       553
Percent Similarity:       100.00%       Conservative:  0
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Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
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Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
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Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
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Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
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Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
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Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
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Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
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Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

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Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
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Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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RESULT 2
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; Sequence 1, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
;  APPLICANT: KAPELLER-LIBERMANN, Rosana
;  APPLICANT:  BANDARU, Rajasekhar
;  TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Proteir
;  TITLE OF INVENTION:  Uses Thereof
;  FILE REFERENCE: 10147-52U1
;  CURRENT APPLICATION NUMBER: US/10/044,205A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: US 60/242,428
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: US 60/241,884
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 60/241,877
;  PRIOR FILING DATE: 2000-10-20
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 2198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-044-205A-1

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Score:                   2889.00        Matches:       553
Percent Similarity:      100.00%        Conservative:  0
Best Local Similarity:   100.00%        Mismatches:    0
Query Match:             100.00%        Indels:        0
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US-10-044-205A-2 (1-553) x US-10-044-205A-1 (1-2198)

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Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
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Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
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Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
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Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
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Db        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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Db        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Db       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1949

RESULT 3
US-10-217-745-1
; Sequence 1, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases anc
;  TITLE OF INVENTION:  Polynucleotides
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/10/217,745
;  CURRENT FILING DATE:  2002-08-12
;  PRIOR APPLICATION NUMBER: US/09/802,117
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-217-745-1

Alignment Scores:
Pred. No.:              0             Length:          1662
Score:                  2883.00       Matches:         552
Percent Similarity:     99.82%        Conservative:    0
Best Local Similarity:  99.82%        Mismatches:      1
Query Match:            99.79%        Indels:          0
DB:                     15            Gaps:            0

US-10-044-205A-2 (1-553) x US-10-217-745-1 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 4
US-10-311-034-45
; Sequence 45, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  YUE, Henry
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  BANDMAN, Olga
;  APPLICANT:  BOROWSKY, Mark L.
;  APPLICANT:  AU-YOUNG, Janice
;  APPLICANT:  LU, Yan
;  APPLICANT:  GANDHI, Ameena R.
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  GREENWALD, Sara R.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  KEARNEY, Liam
;  APPLICANT:  BURFORD, Neil
;  APPLICANT:  NGUYEN, Danniel B.
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  HE, Ann
;  APPLICANT:  THORNTON, Michael
;  APPLICANT:  HAFALIA, April
;  APPLICANT:  ARVIZU, Chandra S.
;  APPLICANT:  GURURAJAN, Rajagopal
;  APPLICANT:  LO, Terence P.
;  APPLICANT:  KHAH, Farrah A.
;  APPLICANT:  RECIPON, Shirley A.
;  APPLICANT:  AZIMZAI, Yalda
;  APPLICANT:  POLICKY, Jennifer L.
;  APPLICANT:  DING, Li
;  APPLICANT:  GRETHER, Megan
;  APPLICANT:  ELLIOTT, Vicki S.
;  APPLICANT:  THANGAVELU, Kavitha
;  APPLICANT:  BATRA, Sajeev
;  APPLICANT:  ISON, Craig H.
;  TITLE OF INVENTION: HUMAN KINASES
;  FILE REFERENCE: PI-0125 PCT
;  CURRENT APPLICATION NUMBER: US/10/311,034
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
;    60/228,056
;  PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
;    25
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PERL Program
; SEQ ID NO 45
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
US-10-311-034-45

Alignment Scores:
Pred. No.:              0             Length:        1662
Score:                  2883.00       Matches:       552
Percent Similarity:     99.82%        Conservative:  0
Best Local Similarity:  99.82%        Mismatches:    1
Query Match:            99.79%        Indels:        0
DB:                     17            Gaps:          0

US-10-044-205A-2 (1-553) x US-10-311-034-45 (1-1662)

Qy           1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy          21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy          61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy          81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy         101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy         121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy         141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
               |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db         421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy         161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy         181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy         201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy         221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy         241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy         261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy         281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy         301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy         341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy         361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy         381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy         401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy         421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy         441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy         461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
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Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 5
US-10-451-168-49
; Sequence 49, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
;  APPLICANT: SMITHKLINE BEECHAM CORPORATION
;  APPLICANT:  SMITHKLINE BEECHAM p.l.c.
;  APPLICANT:  GLAXO GROUP LIMITED
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GP50039
;  CURRENT APPLICATION NUMBER: US/10/451,168
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: PCT/US01/49232
;  PRIOR FILING DATE: 2000-12-17
;  PRIOR APPLICATION NUMBER: 60/256,710
;  PRIOR FILING DATE: 2000-12-19
;  PRIOR APPLICATION NUMBER: 60/257,048
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: 60/260,482
;  PRIOR FILING DATE: 2001-01-09
;  PRIOR APPLICATION NUMBER: 60/264,922
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/266,797
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/276,988
;  PRIOR FILING DATE: 2001-03-19
;  PRIOR APPLICATION NUMBER: 60/281,535
;  PRIOR FILING DATE: 2001-04-04
;  PRIOR APPLICATION NUMBER: 60/289,622
;  PRIOR FILING DATE: 2002-06-28
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-451-168-49

Alignment Scores:
Pred. No.:                0            Length:        1662
Score:                    2883.00      Matches:       552
Percent Similarity:       99.82%       Conservative:  0
Best Local Similarity:    99.82%       Mismatches:    1
Query Match:              99.79%       Indels:        0
DB:                       17           Gaps:          0

US-10-044-205A-2 (1-553) x US-10-451-168-49 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
               |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 6
US-10-217-745-5
; Sequence 5, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases an
;  TITLE OF INVENTION:  Polynucleotides
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/10/217,745
;  CURRENT FILING DATE:  2002-08-12
;  PRIOR APPLICATION NUMBER: US/09/802,117
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 2249
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-217-745-5

Alignment Scores:
Pred. No.:              0              Length:         2249
Score:                  2883.00        Matches:        552
Percent Similarity:     99.82%         Conservative:   0
Best Local Similarity:  99.82%         Mismatches:     1
Query Match:            99.79%         Indels:         0
DB:                     15             Gaps:           0

US-10-044-205A-2 (1-553) x US-10-217-745-5 (1-2249)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 413

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 473

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 533

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 593

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 653

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 713

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 773

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
               |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        774 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 833

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 893

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 953

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 1013

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1014 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1073

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1074 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1133

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1134 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1193

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1194 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1253

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1254 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1313

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1373

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1374 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1433

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1434 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1493

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1494 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1553

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1554 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1613

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1614 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1673

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1674 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1733

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1734 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1793

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1794 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1853

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1854 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1913

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1914 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1974 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 2012
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RESULT 7
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV
;  CURRENT APPLICATION NUMBER: US/09/964,469
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Human
US-09-964-469-1

Alignment Scores:
Pred. No.:                0              Length:        1662
Score:                    2876.00        Matches:       551
Percent Similarity:       99.64%         Conservative:  0
Best Local Similarity:    99.64%         Mismatches:    2
Query Match:              99.55%         Indels:        0
DB:                       9              Gaps:          0

US-10-044-205A-2 (1-553) x US-09-964-469-1 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
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Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
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                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
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RESULT 8
US-10-425-962-1
; Sequence 1, Application US/10425962
; Publication No. US20030180786A1
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV2
;  CURRENT APPLICATION NUMBER: US/10/425,962
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: 09/964,469
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-425-962-1

Alignment Scores:
Pred. No.:              0              Length:        1662
Score:                  2876.00        Matches:       551
Percent Similarity:     99.64%         Conservative:  0
Best Local Similarity:  99.64%         Mismatches:    2
Query Match:            99.55%         Indels:        0
DB:                     15             Gaps:          0

US-10-044-205A-2 (1-553) x US-10-425-962-1 (1-1662).

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
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Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
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RESULT 9
US-10-072-012-273
; Sequence 273, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
;  APPLICANT: Tchernev, Velizar
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Li, Li
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Taupier Jr, Raymond J.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Wolenc, Adam R.
;  APPLICANT:  Pena, Carol E. A
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Grosse, William M.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-258
;  CURRENT APPLICATION NUMBER: US/10/072,012
;  CURRENT FILING DATE:  2002-01-31
;  PRIOR APPLICATION NUMBER: 60/265,102
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/265,514
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,517
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,412
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,395
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/266,406
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/266,767
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: 60/267,057
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/266,975
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/267,459
;  PRIOR FILING DATE: 2001-02-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1391
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
;   LENGTH: 1701
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-072-012-273

Alignment Scores:
Pred. No.:              0              Length:         1701
Score:                  2823.50        Matches:        547
Percent Similarity:     98.56%         Conservative:   0
Best Local Similarity:  98.56%         Mismatches:     1
Query Match:            97.73%         Indels:         7
DB:                     13             Gaps:           3

US-10-044-205A-2 (1-553) x US-10-072-012-273 (1-1701)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
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Db         19 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 78

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 138

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 198

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 258

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 318

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 378

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 438

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        439 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 498

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 558

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 618

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||               |||||||||||||||||||||||||||||||||
Db        619 GGTTTTGGGGAG---------------GTAAAAAACACTGGAAGATGTATGCCTGTAAG 663

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 723

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 783

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 843

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 903

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 963

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1023

Qy        341 MetLysGlyGlyLysProIleThrGlnArg---AlaGlyThrAsnGlyTyrMetAlaPro 359
              ||||||||||||||||||||||||||||||   |||||||||||||||||||||||||||
Db       1024 ATGAAGGGTGGCAAGCCCATCACCCAGAGGCAGGCTGGAACCAATGGTTACATGGCTCCT 1083

Qy        360 GluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCys 379
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGC 1143

Qy        380 SerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSer 399
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1144 AGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGT 1203

Qy        400 LysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPhe 419
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1204 AAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTC 1263

Qy        420 ThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeu 439
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1264 ACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTA 1323

Qy        440 GlySer---ArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsn 458
              ||||||   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 GGAAGCAGGAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAAC 1383

Qy        459 PheProArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValVal 478
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1384 TTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTT 1443

Qy        479 TyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAsp 498
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1444 TATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGAT 1503

Qy        499 AspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGln 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1504 GACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAG 1563

Qy        519 GluGluIleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGly 538
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1564 GAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGT 1623

Qy        539 CysGluGluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1624 TGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1668

RESULT 10
US-10-217-745-3
; Sequence 3, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases anc
;  TITLE OF INVENTION:  Polynucleotides
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/10/217,745
;  CURRENT FILING DATE:  2002-08-12
;  PRIOR APPLICATION NUMBER: US/09/802,117
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1062
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-217-745-3

Alignment Scores:
Pred. No.:              2.44e-215      Length:         1062
Score:                  1801.00        Matches:        349
Percent Similarity:     99.71%         Conservative:   0
Best Local Similarity:  99.71%         Mismatches:     1
Query Match:            62.34%         Indels:         0
DB:                     15             Gaps:           0

US-10-044-205A-2 (1-553) x US-10-217-745-3 (1-1062)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy          221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy          241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy          261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy          281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy          301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy          321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy          341 MetLysGlyGlyLysProIleThrGlnArg 350
                ||||||||||||||||||||||||||||||
Db         1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1050

RESULT 11
US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV
;  CURRENT APPLICATION NUMBER: US/09/964,469
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 36651
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(36651)
;   OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

Alignment Scores:
Pred. No.:                1.32e-178      Length:        36651
Score:                    1528.00        Matches:       349
Percent Similarity:       41.40%         Conservative:  0
Best Local Similarity:    41.40%         Mismatches:    1
Query Match:              52.89%         Indels:        493
DB:                       9              Gaps:          1

US-10-044-205A-2 (1-553) x US-09-964-469-3 (1-36651)

Qy            1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2076 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 2135

Qy           21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2136 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 2195

Qy           41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2196 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 2255

Qy           61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2256 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 2315

Qy           81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2316 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 2375

Qy          101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2376 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 2435

Qy          121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2436 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 2495

Qy          141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
                |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db         2496 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 2555

Qy          161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2556 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 2615

Qy          181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2616 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGAAAGGT 2675

Qy          201 GlyPheGlyGlu------------------------------------------------ 204
                ||||||||||||
Db         2676 GGTTTTGGGGAGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCATAGAGCATGA 2735

Qy          204 ------------------------------------------------------------ 204

Db         2736 AAGGGGGTAATGTTGCCTTTCTTTTTTTAAATCTCAGTTACTTAGAACTAATTTCAGCAC 2795

Qy          204 ------------------------------------------------------------ 204

Db         2796 CATATGTGGAGGATTTCTAGCCCCGTCTCCCCAGCCCCCTTCTTTGTGTGTGCCATGGTG 2855

Qy          204 ------------------------------------------------------------ 204

Db         2856 TGAAATAAAACACAAATGGCATGAGAGAGACAAGCAAAATTTATACTTGGCCAAGACTCT 2915

Qy          204 ------------------------------------------------------------ 204

Db         2916 GTCATGGGTCTCCATTAGGAACGTGCTGAGATGCCTGGACACTTCAGAGAATGATAGCAA 2975

Qy          204 ------------------------------------------------------------ 204

Db         2976 TGTGTGACAGAAGATCTCCGTTTCCCCTAAATTGTGATAATGAAGGCACTTCAAGAAAAA 3035

Qy          204 ------------------------------------------------------------ 204

Db         3036 TGGATATTTAAGAAAATACTCTAACTAGCTGGGTGTGGTGACATGCCTGTAATCCCAGCT 3095

Qy          204 ------------------------------------------------------------ 204

Db         3096 ACTTGGGAGGCTGAAGCAGGAGAATCACTTGAGCCTGGGAGGTGGAGGTTGCAGTGAGCC 3155

Qy          204 ------------------------------------------------------------ 204

Db         3156 AAGATCGTGCCACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCAAAAAAAAAAAAAAA 3215

Qy          204 ------------------------------------------------------------ 204
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Db       3216 AAGAAAGAAAGAAAAGAAAGAAAACACTTATCTTGAAGTAAGGTTGAGAACCTGTTTTGT 3275

Qy        204 ------------------------------------------------------------ 204

Db       3276 ACCACTGTTGTGCCCAGCTTTCTGTTTTTAAGTAATAAAAAATATTTCAGGTAAAATTTG 3335

Qy        204 ------------------------------------------------------------ 204

Db       3336 CTTGATATAAAACTAACCATTAACTGTTTTAAAATGTACAATGCAGTGGCACTTCGCACA 3395

Qy        204 ------------------------------------------------------------ 204

Db       3396 AATGCAATGTTGGGTAAGCAACACCTCAATCTGGATCCAAGACACTCTCATCACCCCTGT 3455

Qy        204 ------------------------------------------------------------ 204

Db       3456 GCCCATTAATAGTGCCTCCCCATCCCTCTCCTCCTCCAGCCCTGACAACCACTAGTCCGC 3515

Qy        204 ------------------------------------------------------------ 204

Db       3516 TTTCTGTCTCTAGGGATTTGCCTATTCTGGGTGTTTCACACAATATGTGACCTTTTGTGT 3575

Qy        204 ------------------------------------------------------------ 204

Db       3576 CTGGCTTCTTTCACTCATTAGAATGTTTTTGGGGTTCATTCACACTGTAGCATGTGTCAA 3635

Qy        204 ------------------------------------------------------------ 204

Db       3636 TACTCCATTCCTTTTTATGGCTGTATAATATTCCATCGTATGGATGTACTACATTTCATG 3695

Qy        204 ------------------------------------------------------------ 204

Db       3696 TAGCCATTCATCTGTTGATGGACACTTGGGCTGTTTTCACCTTTTGGCTATTGTGTATGG 3755

Qy        204 ------------------------------------------------------------ 204

Db       3756 TGCTGCTATTCATGCACAAGTATTTGTTTGAATCCTTGTTTTCATTTCTCTTGGATTTAT 3815

Qy        204 ------------------------------------------------------------ 204

Db       3816 GCCCAGGAGTGGAATTGCTAGGGCATATGGTGATACTATGTTTAACTTTTCAAGGAGCCA 3875

Qy        204 ------------------------------------------------------------ 204

Db       3876 CCAAACTTTCCACATTTTTTATTCCCACCAGCAATGCTTAAAGGTTTCGATTTCTCCACA 3935

Qy        204 ------------------------------------------------------------ 204

Db       3936 TCCTTGCCAACACTTGATATTTTCCTGTATTTTTTTATGAAGGCCTGCCTAGTGAGGTGA 3995

Qy        204 ------------------------------------------------------------ 204

Db       3996 AGGAGTATCGCACTGTAGTCCCCACTTTTTCTTGAGAACACTTCTTATTTACAGCTACTC 4055

Qy        204 ------------------------------------------------------------ 204

Db       4056 CTTTCTCCAATGCCTAACATCTTTCCACCCACCTCCTCCTTTATCATCTCCACCTCTCTG 4115

Qy        205 -------------------------------------------------ValCysAlaVa 208
                                                              |||||||||||
Db       4116 CAGTACCATCTACTTCTACCTCTTTCTCTTCTTTTCTTTCTCCTTTAAGGTATGTGCCGT 4175

Qy        208 lGlnValLysAsnThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLy 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4176 CCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAA 4235

Qy        228 sLysLysGlyGlyGluLysMetAlaLeuLeuGluLysGluIleLeuGluLysValSerSe 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4236 GAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAG 4295

Qy        248 rProPheIleValSerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMe 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4296 CCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCAT 4355
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Qy        268 tSerLeuMetAsnGlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLe 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4356 GAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCT 4415

Qy        288 uAspMetSerArgValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHi 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4416 GGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCA 4475

Qy        308 sGluLeuGlyIleValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGl 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4476 TGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGG 4535

Qy        328 yAsnCysArgLeuSerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleTh 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4536 CAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCAC 4595

Qy        348 rGlnArg 350
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Db       4596 CCAGAGG 4602

RESULT 12
US-10-425-962-3
; Sequence 3, Application US/10425962
; Publication No. US20030180786A1
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV2
;  CURRENT APPLICATION NUMBER: US/10/425,962
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: 09/964,469
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 36651
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(36651)
;   OTHER INFORMATION: n = A,T,C or G
US-10-425-962-3

Alignment Scores:
Pred. No.:              1.32e-178    Length:        36651
Score:                  1528.00      Matches:       349
Percent Similarity:     41.40%       Conservative:  0
Best Local Similarity:  41.40%       Mismatches:    1
Query Match:            52.89%       Indels:        493
DB:                     15           Gaps:          1

US-10-044-205A-2 (1-553) x US-10-425-962-3 (1-36651)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2076 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 2135

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2136 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 2195

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2196 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 2255
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Qy        61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2256 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 2315

Qy        81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2316 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 2375

Qy       101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2376 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 2435

Qy       121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2436 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 2495

Qy       141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
             |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db      2496 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 2555

Qy       161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2556 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 2615

Qy       181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2616 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 2675

Qy       201 GlyPheGlyGlu------------------------------------------------ 204
             ||||||||||||
Db      2676 GGTTTTGGGGAGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCATAGAGCATGA 2735

Qy       204 ------------------------------------------------------------ 204

Db      2736 AAGGGGGTAATGTTGCCTTTCTTTTTTTAAATCTCAGTTACTTAGAACTAATTTCAGCAC 2795

Qy       204 ------------------------------------------------------------ 204

Db      2796 CATATGTGGAGGATTTCTAGCCCCGTCTCCCCAGCCCCCTTCTTTGTGTGTGCCATGGTG 2855

Qy       204 ------------------------------------------------------------ 204

Db      2856 TGAAATAAAACACAAATGGCATGAGAGAGACAAGCAAAATTTATACTTGGCCAAGACTCT 2915

Qy       204 ------------------------------------------------------------ 204

Db      2916 GTCATGGGTCTCCATTAGGAACGTGCTGAGATGCCTGGACACTTCAGAGAATGATAGCAA 2975

Qy       204 ------------------------------------------------------------ 204

Db      2976 TGTGTGACAGAAGATCTCCGTTTCCCCTAAATTGTGATAATGAAGGCACTTCAAGAAAAA 3035

Qy       204 ------------------------------------------------------------ 204

Db      3036 TGGATATTTAAGAAAATACTCTAACTAGCTGGGTGTGGTGACATGCCTGTAATCCCAGCT 3095

Qy       204 ------------------------------------------------------------ 204

Db      3096 ACTTGGGAGGCTGAAGCAGGAGAATCACTTGAGCCTGGGAGGTGGAGGTTGCAGTGAGCC 3155

Qy       204 ------------------------------------------------------------ 204

Db      3156 AAGATCGTGCCACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCAAAAAAAAAAAAAAA 3215

Qy       204 ------------------------------------------------------------ 204

Db      3216 AAGAAAGAAAGAAAAGAAAGAAAACACTTATCTTGAAGTAAGGTTGAGAACCTGTTTTGT 3275

Qy       204 ------------------------------------------------------------ 204

Db      3276 ACCACTGTTGTGCCCAGCTTTCTGTTTTTAAGTAATAAAAAATATTTCAGGTAAAATTTG 3335

Qy       204 ------------------------------------------------------------ 204
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Db      3336 CTTGATATAAAACTAACCATTAACTGTTTTAAAATGTACAATGCAGTGGCACTTCGCACA 3395

Qy       204 ------------------------------------------------------------ 204

Db      3396 AATGCAATGTTGGGTAAGCAACACCTCAATCTGGATCCAAGACACTCTCATCACCCCTGT 3455

Qy       204 ------------------------------------------------------------ 204

Db      3456 GCCCATTAATAGTGCCTCCCCATCCCTCTCCTCCTCCAGCCCTGACAACCACTAGTCCGC 3515

Qy       204 ------------------------------------------------------------ 204

Db      3516 TTTCTGTCTCTAGGGATTTGCCTATTCTGGGTGTTTCACACAATATGTGACCTTTTGTGT 3575

Qy       204 ------------------------------------------------------------ 204

Db      3576 CTGGCTTCTTTCACTCATTAGAATGTTTTTGGGGTTCATTCACACTGTAGCATGTGTCAA 3635

Qy       204 ------------------------------------------------------------ 204

Db      3636 TACTCCATTCCTTTTTATGGCTGTATAATATTCCATCGTATGGATGTACTACATTTCATG 3695

Qy       204 ------------------------------------------------------------ 204

Db      3696 TAGCCATTCATCTGTTGATGGACACTTGGGCTGTTTTCACCTTTTGGCTATTGTGTATGG 3755

Qy       204 ------------------------------------------------------------ 204

Db      3756 TGCTGCTATTCATGCACAAGTATTTGTTTGAATCCTTGTTTTCATTTCTCTTGGATTTAT 3815

Qy       204 ------------------------------------------------------------ 204

Db      3816 GCCCAGGAGTGGAATTGCTAGGGCATATGGTGATACTATGTTTAACTTTTCAAGGAGCCA 3875

Qy       204 ------------------------------------------------------------ 204

Db      3876 CCAAACTTTCCACATTTTTTATTCCCACCAGCAATGCTTAAAGGTTTCGATTTCTCCACA 3935

Qy       204 ------------------------------------------------------------ 204

Db      3936 TCCTTGCCAACACTTGATATTTTCCTGTATTTTTTTATGAAGGCCTGCCTAGTGAGGTGA 3995

Qy       204 ------------------------------------------------------------ 204

Db      3996 AGGAGTATCGCACTGTAGTCCCCACTTTTTCTTGAGAACACTTCTTATTTACAGCTACTC 4055

Qy       204 ------------------------------------------------------------ 204

Db      4056 CTTTCTCCAATGCCTAACATCTTTCCACCCACCTCCTCCTTTATCATCTCCACCTCTCTG 4115

Qy       205 -------------------------------------------------ValCysAlaVa 208
                                                              |||||||||||
Db      4116 CAGTACCATCTACTTCTACCTCTTTCTCTTCTTTTCTTTCTCCTTTAAGGTATGTGCCGT 4175

Qy       208 lGlnValLysAsnThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLy 228
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4176 CCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAA 4235

Qy       228 sLysLysGlyGlyGluLysMetAlaLeuLeuGluLysGluIleLeuGluLysValSerSe 248
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4236 GAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAG 4295

Qy       248 rProPheIleValSerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMe 268
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4296 CCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCAT 4355

Qy       268 tSerLeuMetAsnGlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLe 288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4356 GAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCT 4415

Qy       288 uAspMetSerArgValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHi 308
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4416 GGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCA 4475

Qy        308 sGluLeuGlyIleValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGl 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4476 TGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGG 4535

Qy        328 yAsnCysArgLeuSerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleTh 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4536 CAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGTGGCAAGCCCATCAC 4595

Qy        348 rGlnArg 350
              |||||||
Db       4596 CCAGAGG 4602

RESULT 13
US-10-325-430-2
; Sequence 2, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Rosenfeld, Julie Beth
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
;  TITLE OF INVENTION:  PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
;  TITLE OF INVENTION:  32838,336 and 52908
;  FILE REFERENCE: MPI01-294P1RNM
;  CURRENT APPLICATION NUMBER: US/10/325,430
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/341,953
;  PRIOR FILING DATE: 2001-12-19
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 1737
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1737)
US-10-325-430-2

Alignment Scores:
Pred. No.:                4.67e-150      Length:        1737
Score:                    1283.50        Matches:       255
Percent Similarity:       65.49%         Conservative:  96
Best Local Similarity:    47.57%         Mismatches:    162
Query Match:              44.43%         Indels:        23
DB:                       15             Gaps:          8

US-10-044-205A-2 (1-553) x US-10-325-430-2 (1-1737)

Qy          7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSer---AspCys 25
              |||:::|||::::::||||||:::      |||:::||||||:::
Db          7 CTCGAGAACATCGTGGCCAACTCGCTGCTGCTGAAAGCGCGTCAAGGAGGATATGGCAAA 66

Qy         26 AspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
                 |||         ::::::   :::      |||   ||||||   :::      |||
Db         67 AAAAGTGGTCGTAGTAAAAAATGGAAGGAGATACTGACACTGCCTCCTGTCAGCCAGTGC 126

Qy         46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
              :::|||||||||      :::      ::::::   |||||||||::::::|||||||||
Db        127 AGTGAGCTTAGACATTCCATTGAAAAGGATTATAGCAGTCTTTGTGACAAGCAACCGATA 186

Qy         66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
              ||||||||||||||||||   |||      |||   ||||||   ::::::
Db        187 GGAAGACGTCTCTTCAGGCAGTTCTGTGATACCAAACCCACTCTAAAGAGGCACATTGAA 246

Qy         86 PheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyProThrLysAsp------ 103
              ||||||:::   |||      :::|||:::|||::::::            |||
Db        247 TTCTTGGATGCAGTGGCAGAATATGAAGTTGCCGATGATGAGGACCGAAGTGATTGTGGA 306

Qy        104 ---SerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGlyAsnPro 122
                 |||   |||                        :::||||||   |||      |||
Db        307 CTGTCAATCTTAGATAGATTCTTCAATGATAAGTTGGCAGCCCCTTTACCAGAAATACCT 366

Qy        123 GlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGluGluGlu 142
                                   |||   |||:::|||:::            ||||||
Db        367 CCAGAT---------------GTTGTGACAGAATGTAGATTGGGACTGAAGGAGGAGAAC 411

Qy        143 ArgValAlaAlaValThrLeuArgLysAla------------------GluAlaMetAla 156
                                   :::||||||                     |||
Db        412 ---------------CCTTCCAAAAAAGCCTTTGAGGAATGTACTAGAGTTGCCCATAAC 456

Qy        157 PheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeu 176
              :::|||:::   :::||||||:::::::::      |||:::::::::   :::||||||
Db        457 TACCTAAGAGGGGAACCATTTGAAGAATACCAAGAAAGCTCATATTTTTCTCAGTTTTTA 516

Qy        177 GlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgVal 196
              |||||||||      |||   |||||||||:::         |||      :::||||||
Db        517 CAATGGAAATGGCTGGAAAGGCAACCCGTAACAAAGAACACATTTAGACATTACAGAGTT 576

Qy        197 LeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMet 216
              |||||||||||||||||||||||||||||||||   ||||||:::   ||||||||||||
Db        577 CTAGGAAAAGGCGGATTTGGAGAGGTTTGCGCCTGTCAAGTGCGAGCCACAGGAAAAATG 636

Qy        217 TyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAla 236
              ||||||||||||||||||   |||||||||:::||||||:::   ||||||   ||||||
Db        637 TATGCCTGCAAAAAGCTACAAAAAAAAAGAATAAAGAAGAGGAAAGGTGAAGCTATGGCT 696

Qy        237 LeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyr 256
              |||   ||||||   |||||||||||||||   |||   |||:::|||||||||||||||
Db        697 CTAAATGAGAAAAGAATTCTGGAGAAAGTGCAAAGTAGATTCGTAGTTAGTTTAGCCTAC 756

Qy        257 AlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeu 276
              |||:::|||:::|||      ||||||||||||:::::::::||||||||||||||||||
Db        757 GCTTATGAAACCAAAGATGCCTTGTGCTTGGTGCTCACCATTATGAATGGAGGGGATTTG 816

Qy        277 LysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyr 296
              ||||||||||||||||||:::|||      |||   |||      |||   :::||||||
Db        817 AAGTTTCACATTTACAACCTGGGCAATCCCGGCTTTGATGAGCAGAGAGCCGTTTTCTAT 876

Qy        297 SerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAsp 316
              :::|||::::::   ||||||:::      |||            |||||||||||||||
Db        877 GCTGCAGAGCTGTGTTGCGGCTTGGAAGATTTACAGAGGGAAAGAATTGTATACAGAGAC 936

Qy        317 MetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGly 336
              :::||||||||||||:::||||||||||||   |||:::   |||:::||||||||||||
Db        937 TTGAAGCCTGAGAATATTCTCCTTGATGATCGTGGACACATCCGGATTTCAGACCTCGGT 996

Qy        337 LeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyr 356
              ||||||   |||:::      |||:::   :::      |||   ||||||   ||||||
Db        997 TTGGCCACAGAGATCCCAGAAGGACAGAGGGTTCGAGGAAGAGTTGGAACAGTCGGCTAC 1056

Qy        357 MetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAla 376
              ||||||||||||::::::      :::      |||::::::      ||||||:::
Db       1057 ATGGCACCTGAAGTTGTCAATAATGAA---AAGTATACGTTTAGTCCCGATTGGTGGGGA 1113

Qy        377 MetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlu 396
              :::||||||   ||||||||||||:::   |||   :::|||||||||   |||||||||
Db       1114 CTTGGCTGTCTGATCTATGAAATGATTCAGGGACATTCTCCATTCAAAAAATACAAAGAG 1173

Qy        397 LysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHis 416
              ||||||      |||::::::   ||||||         |||      ::::::
Db       1174 AAAGTCAAATGGGAGGAGGTCGATCAAAGAATCAAGAATGATACCGAGGAGTATTCT--- 1230

Qy        417 AspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGlu 436
              :::   |||:::|||:::||||||   |||||||||:::   |||   |||   |||
Db       1231 GAGAAGTTTTCAGAGGATGCCAAATCTATCTGCAGGATGTTACTCACCAAGAATCCAAGC 1290

Qy        437 GlnArgLeuGlySerArg---GluLysSerAspAspProArgLysHisHisPhePheLys 455
              :::|||||||||   |||   |||   :::         ::::::|||      ||||||
Db       1291 AAGCGGCTGGGCTGCAGGGGCGAGGAGCGGCTGGGGTGAAGCAGCACCCCGTGTTCAAG 1350

Qy        456 ThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAspPro 475
                 |||||||||   ||||||||||||   ::::::||||||||||||   |||||||||
Db       1351 GACATCAACTTCAGGAGGCTGGAGGCAAACATGCTGGAGCCCCCTTTCTGTCCTGATCCT 1410
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Qy           476 SerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGlyVal 495
                       ||||||   ||||||:::   :::|||:::   ||||||   |||:::|||:::
Db          1411 CATGCCGTTTACTGTAAGGACGTCCTGGATATCGAGCAGTTCTCGGCGGTGAAAGGGATC 1470

Qy           496 GluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIle 515
                       |||      |||:::   |||:::      ||||||||||||   |||   |||
Db          1471 TACCTGGACACCGCAGATGAAGACTTCTATGCTCGGTTTGCTACCGGGTGTGTCTCCATC 1530

Qy           516 AlaTrpGlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
                    ||||||   |||:::||||||:::|||   |||:::::::::|||
Db          1531 CCCTGGCAGAATGAGATGATCGAATCCGGGTGTTTCAAAGACATCAAC 1578

RESULT 14
US-10-325-430-1
; Sequence 1, Application US/10325430
; Publication No. US20030153525A1
; GENERAL INFORMATION:
;  APPLICANT: Millennium Pharmaceuticals, Inc
;  APPLICANT:  Silos-Santiago, Inmaculada
;  APPLICANT:  Rosenfeld, Julie Beth
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS IN TREATING
;  TITLE OF INVENTION:  PAIN AND PAINFUL DISORDERS USING 1465, 1587, 2146, 2207,
;  TITLE OF INVENTION:  32838,336 and 52908
;  FILE REFERENCE: MPI01-294P1RNM
;  CURRENT APPLICATION NUMBER: US/10/325,430
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US 60/341,953
;  PRIOR FILING DATE: 2001-12-19
;  NUMBER OF SEQ ID NOS: 21
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 2113
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
US-10-325-430-1

Alignment Scores:
Pred. No.:              6.41e-150       Length:         2113
Score:                  1283.50         Matches:        255
Percent Similarity:     65.49%          Conservative:   96
Best Local Similarity:  47.57%          Mismatches:     162
Query Match:            44.43%          Indels:         23
DB:                     15              Gaps:           8

US-10-044-205A-2 (1-553) x US-10-325-430-1 (1-2113)

Qy             7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSer---AspCys 25
                 |||:::|||::::::||||||:::      |||:::||||||:::
Db           261 CTCGAGAACATCGTGGCCAACTCGCTGCTGCTGAAAGCGCGTCAAGGAGGATATGGCAAA 320

Qy            26 AspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
                    |||         ::::::   :::      |||   ||||||   :::      |||
Db           321 AAAAGTGGTCGTAGTAAAAAATGGAAGGAGATACTGACACTGCCTCCTGTCAGCCAGTGC 380

Qy            46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
                 :::|||||||||      :::      ::::::   |||||||||::::::|||||||||
Db           381 AGTGAGCTTAGACATTCCATTGAAAAGGATTATAGCAGTCTTTGTGACAAGCAACCGATA 440

Qy            66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
                 ||||||||||||||||||   |||      |||   ||||||   ::::::
Db           441 GGAAGACGTCTCTTCAGGCAGTTCTGTGATACCAAACCCACTCTAAAGAGGCACATTGAA 500

Qy            86 PheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyProThrLysAsp------ 103
                 ||||||:::   |||      :::|||:::|||::::::            |||
Db           501 TTCTTGGATGCAGTGGCAGAATATGAAGTTGCCGATGATGAGGACCGAAGTGATTGTGGA 560

Qy           104 ---SerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGlyAsnPro 122
                    |||   |||                        :::||||||   |||      |||
Db           561 CTGTCAATCTTAGATAGATTCTTCAATGATAAGTTGGCAGCCCCTTTACCAGAAATACCT 620

Qy           123 GlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGluGluGlu 142
                                      |||   |||:::|||:::            ||||||
Db           621 CCAGAT---------------GTTGTGACAGAATGTAGATTGGGACTGAAGGAGGAGAAC 665

Qy           143 ArgValAlaAlaValThrLeuArgLysAla------------------GluAlaMetAla 156
                                      :::||||||                     |||
Db           666 ---------------CCTTCCAAAAAAGCCTTTGAGGAATGTACTAGAGTTGCCCATAAC 710

Qy           157 PheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeu 176
                 :::|||:::   :::||||||:::::::::      |||:::::::::   :::||||||
Db           711 TACCTAAGAGGGGAACCATTTGAAGAATACCAAGAAAGCTCATATTTTTCTCAGTTTTTA 770

Qy           177 GlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgVal 196
                 |||||||||      |||   |||||||||:::         |||      :::||||||
Db           771 CAATGGAAATGGCTGGAAAGGCAACCCGTAACAAAGAACACATTTAGACATTACAGAGTT 830

Qy           197 LeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMet 216
                 |||||||||||||||||||||||||||||||||   ||||||:::   ||||||||||||
Db           831 CTAGGAAAAGGCGGATTTGGAGAGGTTTGCGCCTGTCAAGTGCGAGCCACAGGAAAAATG 890

Qy           217 TyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAla 236
                 ||||||||||||||||||   |||||||||:::||||||:::   ||||||   ||||||
Db           891 TATGCCTGCAAAAAGCTACAAAAAAAAAGAATAAAGAAGAGGAAAGGTGAAGCTATGGCT 950

Qy           237 LeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyr 256
                 |||   ||||||   |||||||||||||||   |||   |||:::|||||||||||||||
Db           951 CTAAATGAGAAAAGAATTCTGGAGAAAGTGCAAAGTAGATTCGTAGTTAGTTTAGCCTAC 1010

Qy           257 AlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeu 276
                 |||:::|||:::|||      ||||||||||||:::::::::||||||||||||||||||
Db          1011 GCTTATGAAACCAAAGATGCCTTGTGCTTGGTGCTCACCATTATGAATGGAGGGGATTTG 1070

Qy           277 LysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyr 296
                 ||||||||||||||||||:::|||      |||   |||      |||   :::||||||
Db          1071 AAGTTTCACATTTACAACCTGGGCAATCCCGGCTTTGATGAGCAGAGAGCCGTTTTCTAT 1130

Qy           297 SerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAsp 316
                 :::|||::::::   ||||||:::      |||            |||||||||||||||
Db          1131 GCTGCAGAGCTGTGTTGCGGCTTGGAAGATTTACAGAGGGAAAGAATTGTATACAGAGAC 1190

Qy           317 MetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGly 336
                 :::||||||||||||:::||||||||||||   |||:::   |||:::||||||||||||
Db          1191 TTGAAGCCTGAGAATATTCTCCTTGATGATCGTGGACACATCCGGATTTCAGACCTCGGT 1250

Qy           337 LeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyr 356
                 ||||||   |||:::      |||:::   :::      |||   ||||||   ||||||
Db          1251 TTGGCCACAGAGATCCCAGAAGGACAGAGGGTTCGAGGAAGAGTTGGAACAGTCGGCTAC 1310

Qy           357 MetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAla 376
                 ||||||||||||::::::      :::      |||::::::      ||||||:::
Db          1311 ATGGCACCTGAAGTTGTCAATAATGAA---AAGTATACGTTTAGTCCCGATTGGTGGGGA 1367

Qy           377 MetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlu 396
                 :::||||||   ||||||||||||:::   |||   :::|||||||||   |||||||||
Db          1368 CTTGGCTGTCTGATCTATGAAATGATTCAGGGACATTCTCCATTCAAAAAATACAAAGAG 1427

Qy           397 LysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHis 416
                 ||||||      |||::::::   ||||||         |||      ::::::
Db          1428 AAAGTCAAATGGAGGAGGTCGATCAAAGAATCAAGAATGATACCGAGGAGTATTCT--- 1484

Qy           417 AspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGlu 436
                 :::   |||:::|||:::||||||   |||||||||:::   |||   |||   |||
Db          1485 GAGAAGTTTTCAGAGGATGCCAAATCTATCTGCAGGATGTTACTCACCAAGAATCCAAGC 1544

Qy           437 GlnArgLeuGlySerArg---GluLysSerAspAspProArgLysHisHisPhePheLys 455
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Db          1545 AAGCGGCTGGGCTGCAGGGGCGAGGGAGCGGCTGGGGTGAAGCAGCACCCCGTGTTCAAG 1604

Qy           456 ThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAspPro 475
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Db          1605 GACATCAACTTCAGGAGGCTGGAGGCAAACATGCTGGAGCCCCCTTTCTGTCCTGATCCT 1664

Qy           476 SerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGlyVal 495
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Qy        496 GluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIle 515
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Qy        516 AlaTrpGlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
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; Sequence 110, Application US/10084817
; Publication No. US20030119009A1
; GENERAL INFORMATION:
;  APPLICANT: Susan Stuart
;  APPLICANT:  Jed G. Nuchtern
;  APPLICANT:  Sharon E. Plon
;  APPLICANT:  Jason M. Shohet
;  TITLE OF INVENTION: GENES REGULATED BY MYCN ACTIVATION
;  FILE REFERENCE: PA-0046 US
;  CURRENT APPLICATION NUMBER: US/10/084,817
;  CURRENT FILING DATE:  2002-02-25
;  PRIOR APPLICATION NUMBER: 60/270,784
;  PRIOR FILING DATE: 2001-02-23
;  NUMBER OF SEQ ID NOS: 365
;  SOFTWARE: PERL Program
; SEQ ID NO 110
;   LENGTH: 2467
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20030119009A1 875668CB1
US-10-084-817-110

Alignment Scores:
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US-10-044-205A-2 (1-553) x US-10-084-817-110 (1-2467)

Qy          7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSerAspCysAsp 26
              |||:::|||::::::|||||||||      |||:::||||||:::
Db        134 CTGGAAAACATCGTGGCCAACACGGTCTTGCTGAAAGCCAGGGAAGGGGGCGGAGGAAAG 193

Qy         27 SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
                 |||         ::::::   :::      |||      |||   :::      |||
Db        194 CGCAAAGGGAAAAGCAAGAAGTGGAAAGAAATCCTGAAGTTCCCTCACATTAGCCAGTGT 253

Qy         46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
                 :::||||||:::   :::         ::::::   |||||||||::::::|||||||||
Db        254 GAAGACCTCCGAAGGACCATAGACAGAGATTACTGCAGTTTATGTGACAAGCAGCCAATC 313

Qy         66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
              ||||||   |||||||||   |||      |||   |||
Db        314 GGGAGGCTGCTTTTCCGGCAGTTTTGTGAAACCAGGCCTGGGCTGGAGTGTTACATTCAG 373

Qy         86 PheLeuGluAspValGlnAsnTrpGlu------------------LeuAlaGluGluGly 99
              ||||||:::   |||      :::|||                  |||   |||:::|||
Db        374 TTCCTGGACTCCGTGGCAGAATATGAAGTTACTCCAGATGAAAAACTGGGAGAGAAAGGG 433

Qy        100 ProThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaPro 119
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Db        434 ------AAGGAAATTATGACCAAGTACCTC------------------------ACCCCA 463

Qy        120 GlyAsnPro---------------------GlnProPheLeuSerGlnAlaValAlaThr 132
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Db        464 AAGTCCCCTGTTTTCATAGCCCAAGTTGGCCAAGACCTGGTCTCCCAGACGGAGGAGAAG 523
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Qy        133 LysCysGlnAlaAlaThrThrGluGluGluArgValAlaAlaValThrLeuArgLysAla 152
                    |||            |||               |||   ::::::   :::
Db        524 CTCCTACAGAAGCCGTGCAAAGAACTCTTTTCTGCCTGTGCACAGTCTGTCCACGAG--- 580

Qy        153 GluAlaMetAlaPheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyr 172
                          :::|||:::   :::||||||   :::::::::   |||   |||:::
Db        581 ------------TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTT 628

Qy        173 AspLysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThr 192
              |||:::|||||||||||||||      |||   |||||||||:::         |||
Db        629 GACCGCTTTCTCCAGTGGAAGTGGTTGGAAAGGCAACCGGTGACCAAAAACAATTTCAGG 688

Qy        193 GluPheArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsn 212
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Db        689 CAGTATCGAGTGCTAGGAAAAGGGGGCTTCGGGGAGGTCTGTGCCTGCCAGGTTCGGGCC 748

Qy        213 ThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGly 232
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Db        749 ACGGGTAAAATGTATGCCTGCAAGCGCTTGGAGAAGAAGAGGATCAAAAAGAGGAAAGGG 808

Qy        233 GluLysMetAlaLeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleVal 252
              |||   |||||||||   ||||||:::|||||||||||||||:::|||   |||:::|||
Db        809 GAGTCCATGGCCCTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTC 868

Qy        253 SerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsn 272
              :::||||||||||||:::|||:::|||      ||||||||||||:::::::::||||||
Db        869 AACCTGGCCTATGCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAAT 928

Qy        273 GlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArg 292
              ||||||||||||||||||||||||||||||:::|||      |||   :::      |||
Db        929 GGGGGTGACCTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGG 988

Qy        293 ValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIle 312
                 :::||||||:::|||:::|||   ||||||:::      ||||||
Db        989 GCCTTGTTTTATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACC 1048

Qy        313 ValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeu 332
              ||||||||||||:::||||||||||||:::||||||||||||   |||:::   |||:::
Db       1049 GTCTACCGAGATCTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATC 1108

Qy        333 SerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGly 352
              |||||||||||||||||||||::::::      |||      |||      |||   |||
Db       1109 TCAGACCTGGGCTTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGC 1168

Qy        353 ThrAsnGlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProVal 372
              |||   ||||||||||||||||||:::|||      :::      |||
Db       1169 ACTGTTGGCTACATGGCTCCAGAGGTCCTGAACAACCAG---AGGTACGGCCTGAGCCCC 1225

Qy        373 AspTrpPheAlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLys 392
              |||::::::   :::||||||   ||||||||||||:::   |||::::::||||||:::
Db       1226 GACTACTGGGGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGC 1285

Qy        393 AspTyrLysGluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluVal 412
                    ||||||||||||   :::|||::::::   :::|||   |||:::   |||
Db       1286 GGCCGCAAGGAGAAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGGAGGAG 1345

Qy        413 LysPheGlnHisAspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAla 432
                 :::   |||      |||:::||||||||||||   ||||||::::::   |||
Db       1346 GTGTACTCCCAC---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACG 1402

Qy        433 LysLysProGluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHis 451
              |||      :::||||||||||||   :::|||:::   :::   :::   ::::::|||
Db       1403 AAAGATGCGAAGCAGAGGCTGGGCTGCCAGGAGGAGGGGGCTGCAGAGGTCAAGAGACAC 1462

Qy        452 HisPhePheLysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPhe 471
                 ||||||:::   :::||||||   |||||||||||||||:::::::::|||||||||
Db       1463 CCCTTCTTCAGGAACATGAACTTCAAGCGCTTAGAAGCCGGGATGTTGGACCCTCCCTTC 1522

Qy        472 ValProAspProSerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGlu 491
              ||||||||||||      ||||||   ||||||:::   :::|||:::   ||||||
Db       1523 GTTCCAGACCCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACT 1582

Qy        492 ValArgGlyValGluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGly 511
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             |||:::||||||      |||      |||      |||:::      |||:::||||||
Db      1583 GTGAAGGGCGTCAATCTGGACCACACAGACGACGACTTCTACTCCAAGTTCTCCACGGGC 1642

Qy       512 AlaValProIleAlaTrpGlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
             :::|||   |||   ||||||   |||:::|||||||||      |||:::|||||||||
Db      1643 TCTGTGTCCATCCCATGGCAAAACGAGATGATAGAAACAGAATGCTTTAAGGAGCTGAAC 1702

Qy       532 ------------------------------------------------AspPro-AsnAr 535
                                                                |||-|||||
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Search completed: August 13, 2004, 21:21:52
Job time : 573 secs
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                        GenCore version 5.1.6
              Copyright (c) 1993 - 2004  Compugen Ltd.


OM protein - nucleic search, using frame_plus_p2n model

Run on:         August 13, 2004, 17:28:46 ; Search time 4223 Seconds
                                             (without alignments)
                                             5675.751 Million cell updates/sec

Title:          US-10-044-205A-2
Perfect score:  2889
Sequence:       1 MVDMGALDNLIANTAYLQAR..........NRPTGCEEGNSSKSGVCLLL 553

Scoring table:  BLOSUM62
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Searched:       3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US10044205/runat_06082004_104322_23357/app_query.fasta_1.711
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

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                                   ALIGNMENTS

RESULT 1
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DEFINITION  Sequence 3 from Patent WO02095032.
ACCESSION   AX797554
VERSION     AX797554.1  GI:37518056
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kapeller-Libermann,R. and Bandaru,R.
  TITLE     Method and compositions of human proteins and uses thereof
  JOURNAL   Patent: WO 02095032-A 3 28-NOV-2002;
            MILLENIUM PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              7.03e-251      Length:         1659
Score:                  2889.00        Matches:        553
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     6              Gaps:           0

US-10-044-205A-2 (1-553) x AX797554 (1-1659)

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Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
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Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
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Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
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Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
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Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 2
AX797552
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LOCUS       AX797552                2198 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 1 from Patent WO02095032.
ACCESSION   AX797552
VERSION     AX797552.1  GI:37518055
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kapeller-Libermann,R. and Bandaru,R.
  TITLE     Method and compositions of human proteins and uses thereof
  JOURNAL   Patent: WO 02095032-A 1 28-NOV-2002;
            MILLENIUM PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1..2198
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.01e-250      Length:        2198
Score:                  2889.00        Matches:       553
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     6              Gaps:          0

US-10-044-205A-2 (1-553) x AX797552 (1-2198)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Db        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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Db       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
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Db       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
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Db       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1949

RESULT 3
AR225817
LOCUS       AR225817                1662 bp    DNA     linear   PAT 20-DEC-2002
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DEFINITION  Sequence 1 from patent US 6444456.
ACCESSION   AR225817
VERSION     AR225817.1  GI:27263947
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1662)
  AUTHORS   Walke,D.W., Wilganowski,N.L. and Turner,C.A. Jr.
  TITLE     Human G-coupled protein receptor kinases and polynucleotides
            encoding the same
  JOURNAL   Patent: US 6444456-A 1 03-SEP-2002;
FEATURES             Location/Qualifiers
     source          1..1662
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.45e-250       Length:         1662
Score:                  2883.00         Matches:        552
Percent Similarity:     99.82%          Conservative:   0
Best Local Similarity:  99.82%          Mismatches:     1
Query Match:            99.79%          Indels:         0
DB:                     6               Gaps:           0

US-10-044-205A-2 (1-553) x AR225817 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
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Db          1 ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
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Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 4
AX252439
LOCUS       AX252439                1662 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 1 from Patent WO0168869.
ACCESSION   AX252439
VERSION     AX252439.1  GI:15985733
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KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Walke,D.W., Wilganowski,N.L. and Turner,C.A.
  TITLE     Human g-coupled protein receptor kinases and polynucleotides
            encoding the same
  JOURNAL   Patent: WO 0168869-A 1 20-SEP-2001;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
     source          1..1662
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              2.45e-250      Length:         1662
Score:                  2883.00        Matches:        552
Percent Similarity:     99.82%         Conservative:   0
Best Local Similarity:  99.82%         Mismatches:     1
Query Match:            99.79%         Indels:         0
DB:                     6              Gaps:           0

US-10-044-205A-2 (1-553) x AX252439 (1-1662)

Qy           1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy          21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy          61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy          81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy         101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy         121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy         141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
               |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db         421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy         161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Db         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy         181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
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Db         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy         201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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Db         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy         221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Db         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy         241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Db         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy         261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy         281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy         301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
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Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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Db         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy         341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy         361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Db        1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy         381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
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Db        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy         401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
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Db        1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy         421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy         441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
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Db        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy         461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
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Db        1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy         481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
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Db        1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy         501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy         521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
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Db        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy         541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
               |||||||||||||||||||||||||||||||||||||||
Db        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 5
AX642968
LOCUS       AX642968                1662 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 45 from Patent WO01096547.
ACCESSION   AX642968
VERSION     AX642968.1  GI:28550117
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KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,
            Gandhi,A.R., Tribouley,C.M., Walia,N., Yao,M.G., Lu,D.A.,
            Greenwald,S.R., Ramkumar,J., Griffin,J.A., Kearney,L., Burford,N.,
            Nguyen,D.B., Tang,Y.T., Baughn,M.R., He,A., Thornton,M.,
            Hafalia,A., Patterson,C., Gururajan,R., Lo,T.P., Khan,F.,
            Recipon,S.A., Azimzai,Y., Policky,J.L., Ding,L., Grether,M.,
            Elliott,V.S., Thangavelu,K., Batra,S. and Ison,C.H.
  TITLE     Humain kinases
  JOURNAL   Patent: WO 01096547-A 45 20-DEC-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1662
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
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                     /note="Incyte ID No: 7477204CB1"
ORIGIN

Alignment Scores:
Pred. No.:              2.45e-250       Length:         1662
Score:                  2883.00         Matches:        552
Percent Similarity:     99.82%          Conservative:   0
Best Local Similarity:  99.82%          Mismatches:     1
Query Match:            99.79%          Indels:         0
DB:                     6               Gaps:           0

US-10-044-205A-2 (1-553) x AX642968 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
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Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
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Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
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Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
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Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
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Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
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Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
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Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
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Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
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Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
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Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
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Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
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Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
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Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
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RESULT 6
BD186115
LOCUS       BD186115                1761 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  A novel gene relating to disease and use thereof.
ACCESSION   BD186115
VERSION     BD186115.1  GI:31878315
KEYWORDS    WO 02103020-A/10.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1761)
  AUTHORS   Koyama,N., Tanida,S. and Yamamoto,K.
  TITLE     A novel gene relating to disease and use thereof
  JOURNAL   Patent: WO 02103020-A 10 27-DEC-2002;
            TAKEDA CHEMICAL INDUSTRIES LTD,NOBUYUKI KOYAMA,SEIICHI TANIDA,KOJI
            YAMAMOTO
COMMENT     OS   Homo sapiens (human)
            PN   WO 02103020-A/10
            PD   27-DEC-2002
            PF   14-JUN-2002 WO 2002JP005942
            PR   15-JUN-2001 JP 01P   182654
            PI   NOBUYUKI KOYAMA,SEIICHI TANIDA,KOJI YAMAMOTO
            PC   C12N15/54,C12N9/12,G01N33/50,G01N33/15,C07K16/40,A61K39/395 CC
               A novel gene relating to disease and use thereof FH    Key
               Location/Qualifiers
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FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              2.64e-250      Length:        1761
Score:                  2883.00        Matches:       552
Percent Similarity:     99.82%         Conservative:  0
Best Local Similarity:  99.82%         Mismatches:    1
Query Match:            99.79%         Indels:        0
DB:                     6              Gaps:          0

US-10-044-205A-2 (1-553) x BD186115 (1-1761)

Qy           1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
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Db          26 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 85

Qy          21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
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Db          86 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 145

Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
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Qy          61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
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Db         206 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 265

Qy          81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
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Db         266 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 325

Qy         101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
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Db         326 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 385

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Qy         141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
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Db         446 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 505

Qy         161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Qy         181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
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Qy         201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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Db         626 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 685

Qy         221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Qy         241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Qy         361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Qy         461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
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Qy         521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
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Qy         541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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RESULT 7
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LOCUS       AF439409                1799 bp    mRNA    linear   PRI 21-FEB-2002
DEFINITION  Homo sapiens G-protein-coupled receptor kinase 7 (GRK7) mRNA,
            GRK7-S allele, complete cds.
ACCESSION   AF439409
VERSION     AF439409.1  GI:17933258
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1799)
  AUTHORS   Chen,C.K., Zhang,K., Church-Kopish,J., Huang,W., Zhang,H.,
            Chen,Y.J., Frederick,J.M. and Baehr,W.
  TITLE     Characterization of human GRK7 as a potential cone opsin kinase
  JOURNAL   Mol. Vis. 7, 305-313 (2001)
  MEDLINE   21626361
   PUBMED   11754336
REFERENCE   2  (bases 1 to 1799)
  AUTHORS   Baehr,W. and Chen,C.-K.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2001) Ophthalmology, University of Utah, 15
            North/2030 East, Salt Lake City, UT 84112, USA
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ORIGIN

Alignment Scores:
Pred. No.:              2.71e-250      Length:        1799
Score:                  2883.00        Matches:       552
Percent Similarity:     99.82%         Conservative:  0
Best Local Similarity:  99.82%         Mismatches:    1
Query Match:            99.79%         Indels:        0
DB:                     9              Gaps:          0

US-10-044-205A-2 (1-553) x AF439409 (1-1799)
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Qy           1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
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Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
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Db         378 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 437

Qy         101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
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Db         438 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 497

Qy         121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
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Db         498 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 557

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Db         558 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 617

Qy         161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Qy         201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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Db         738 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 797

Qy         221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Qy         241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Qy         261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
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Qy         341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
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Db       1278 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1337

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Db       1338 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1397

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
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RESULT 8
AR225819
LOCUS       AR225819                2249 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6444456.
ACCESSION   AR225819
VERSION     AR225819.1  GI:27263949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2249)
  AUTHORS   Walke,D.W., Wilganowski,N.L. and Turner,C.A. Jr.
  TITLE     Human G-coupled protein receptor kinases and polynucleotides
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  JOURNAL   Patent: US 6444456-A 5 03-SEP-2002;
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ORIGIN

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Best Local Similarity:    99.82%         Mismatches:      1
Query Match:              99.79%         Indels:          0
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US-10-044-205A-2 (1-553) x AR225819 (1-2249)

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Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
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Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
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Db        834 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 893

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 953

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 1013

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Db       1014 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1073

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Db       1074 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1133

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
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Db       1134 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1193

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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Db       1194 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1253

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
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Db       1254 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1313

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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Db       1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1373

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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Db       1374 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1433

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Db       1434 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1493
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Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
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Db       1494 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1553

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1554 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1613

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1614 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1673

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
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Db       1674 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1733

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1734 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1793

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1794 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1853

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1854 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1913

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1914 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1974 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 2012

RESULT 9
AX252443
LOCUS       AX252443                2249 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 5 from Patent WO0168869.
ACCESSION   AX252443
VERSION     AX252443.1  GI:15985735
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Walke,D.W., Wilganowski,N.L. and Turner,C.A.
  TITLE     Human g-coupled protein receptor kinases and polynucleotides
            encoding the same
  JOURNAL   Patent: WO 0168869-A 5 20-SEP-2001;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
     source          1..2249
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              3.62e-250       Length:         2249
Score:                  2883.00         Matches:        552
Percent Similarity:     99.82%          Conservative:   0
Best Local Similarity:  99.82%          Mismatches:     1
Query Match:            99.79%          Indels:         0
DB:                     6               Gaps:           0

US-10-044-205A-2 (1-553) x AX252443 (1-2249)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 413

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 473

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 533

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 593

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 653

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 713

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 773

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        774 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 833

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Db        834 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 893

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGAAAGGT 953

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 1013

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Db       1014 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1073

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Db       1074 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1133

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
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Db       1134 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1193

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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Db       1194 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1253

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
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Db       1254 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1313

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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Db       1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1373

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1374 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1433

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Db       1434 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1493
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Qy         381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
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Db        1494 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1553

Qy         401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1554 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1613

Qy         421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1614 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1673

Qy         441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
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Db        1674 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1733

Qy         461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
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Db        1734 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1793

Qy         481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
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Db        1794 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1853

Qy         501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1854 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1913

Qy         521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1914 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973

Qy         541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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Db        1974 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 2012

RESULT 10
AX710216
LOCUS       AX710216                3186 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 4 from Patent WO03018815.
ACCESSION   AX710216
VERSION     AX710216.1  GI:29786804
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human g protein-couple receptor kinase
  JOURNAL   Patent: WO 03018815-A 4 06-MAR-2003;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
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Alignment Scores:
Pred. No.:              5.69e-250       Length:         3186
Score:                  2883.00         Matches:        552
Percent Similarity:     99.82%          Conservative:   0
Best Local Similarity:  99.82%          Mismatches:     1
Query Match:            99.79%          Indels:         0
DB:                     6               Gaps:           0

US-10-044-205A-2 (1-553) x AX710216 (1-3186)

Qy           1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          85 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 144

Qy          21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
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Db         145 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 204

Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
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Db         205 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 264

Qy          61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
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Db         265 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 324

Qy          81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         325 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 384

Qy         101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         385 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 444

Qy         121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         445 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 504

Qy         141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
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Db         505 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 564

Qy         161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Db         565 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 624

Qy         181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
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Db         625 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 684

Qy         201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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Qy         221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Db         745 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 804

Qy         241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Db         805 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 864

Qy         261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
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Db         865 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 924

Qy         281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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Db         925 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 984

Qy         301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         985 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1044

Qy         321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1045 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1104

Qy         341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1105 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1164

Qy         361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1165 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1224
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Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1225 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1284

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1285 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1344

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1345 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1404

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1405 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1464

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1465 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1524

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1525 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1584

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1585 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1644

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1645 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1704

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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Db       1705 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1743

RESULT 11
AF282269
LOCUS       AF282269                3186 bp    mRNA    linear   PRI 21-NOV-2001
DEFINITION  Homo sapiens G protein-coupled receptor kinase 7 mRNA, complete
            cds.
ACCESSION   AF282269
VERSION     AF282269.1  GI:17026317
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3186)
  AUTHORS   Weiss,E.R., Ducceschi,M.H., Horner,T.J., Li,A., Craft,C.M. and
            Osawa,S.
  TITLE     Species-specific differences in expression of G-protein-coupled
            receptor kinase (GRK) 7 and GRK1 in mammalian cone photoreceptor
            cells: implications for cone cell phototransduction
  JOURNAL   J. Neurosci. 21 (23), 9175-9184 (2001)
  MEDLINE   21574315
   PUBMED   11717351
REFERENCE   2  (bases 1 to 3186)
  AUTHORS   Osawa,S. and Weiss,E.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Cell Biology and Anatomy, University of
            North Carolina, CB#7090, 108 Taylor Hall, Chapel Hill, NC
            27599-7090, USA
FEATURES             Location/Qualifiers
     source          1. .3186
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
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                     /note="protein kinase; GRK7"
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                     /protein_id="AAL33880.1"
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                     QPFKDFVTSAFYDKFLQWKLFEMQPVSDKYFTEFRVLGKGGFGEVCAVQVKNTGKMYA
                     CKKLDKKRLKKKGGEKMALLEKEILEKVSSPFIVSLAYAFESKTHLCLVMSLMNGGDL
                     KFHIYNVGTRGLDMSRVIFYSAQIACGMLHLHELGIVYRDMKPENVLLDDLGNCRLSD
                     LGLAVEMKGGKPITQRAGTNGYMAPEILMEKVSYSYPVDWFAMGCSIYEMVAGRTPFK
                     DYKEKVSKEDLKQRTLQDEVKFQHDNFTEEAKDICRLFLAKKPEQRLGSREKSDDPRK
                     HHFFKTINFPRLEAGLIEPPFVPDPSVVYAKDIAEIDDFSEVRGVEFDDKDKQFFKNF
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ORIGIN

Alignment Scores:
Pred. No.:              5.69e-250      Length:         3186
Score:                  2883.00        Matches:        552
Percent Similarity:     99.82%         Conservative:   0
Best Local Similarity:  99.82%         Mismatches:     1
Query Match:            99.79%         Indels:         0
DB:                     9              Gaps:           0

US-10-044-205A-2 (1-553) x AF282269 (1-3186)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 144

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 204

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 264

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 324

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 384

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 444

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 504

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        505 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 564

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 624

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 684

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 744

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 804

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Db        805 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 864

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 924

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 984

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1044

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1045 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1104

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1164

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1165 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1224

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1225 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1284

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1285 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1344

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1345 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1404

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1405 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1464

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
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Db       1465 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1524

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1525 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1584

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1585 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1644

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
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Db       1645 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1704

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1705 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1743

RESULT 12
AR263766
LOCUS       AR263766                1662 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 1 from patent US 6331423.
ACCESSION   AR263766
VERSION     AR263766.1  GI:28075747
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1662)
  AUTHORS   Guegler,K., Beasley,E.M. and Di Francesco,V.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: US 6331423-A 1 18-DEC-2001;
FEATURES             Location/Qualifiers
     source          1. .1662
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.05e-249       Length:.        1662
Score:                  2876.00         Matches:        551
Percent Similarity:     99.64%          Conservative:   0
Best Local Similarity:  99.64%          Mismatches:     2
Query Match:            99.55%          Indels:         0
DB:                     6               Gaps:           0

US-10-044-205A-2 (1-553) x AR263766 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
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Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
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Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
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Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
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Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
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Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 13
AR343544
LOCUS       AR343544                1662 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6579709.
ACCESSION   AR343544
VERSION     AR343544.1  GI:33739257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1662)
  AUTHORS   Guegler,K., Beasley,E.M. and Di Francesco,V.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: US 6579709-A 1 17-JUN-2003;
FEATURES             Location/Qualifiers
     source          1..1662
                     /organism="unknown"
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ORIGIN

Alignment Scores:
Pred. No.:             1.05e-249      Length:        1662
Score:                 2876.00        Matches:       551
Percent Similarity:    99.64%         Conservative:  0
Best Local Similarity: 99.64%         Mismatches:    2
Query Match:           99.55%         Indels:        0
DB:                    6              Gaps:          0

US-10-044-205A-2 (1-553) x AR343544 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
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Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
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Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGAGACCTCAAGTTCCACATC 840
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Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 14
AX357902
LOCUS       AX357902                1662 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 1 from Patent WO0192496.
ACCESSION   AX357902
VERSION     AX357902.1  GI:18674690
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Guegler,K., di Francesco,V. and Beasley,E.M.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: WO 0192496-A 1 06-DEC-2001;
            Applera Corporation Robert A. Millman Assistant Secretary (US)
FEATURES             Location/Qualifiers
     source          1. .1662
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              1.05e-249       Length:         1662
Score:                  2876.00         Matches:        551
Percent Similarity:     99.64%          Conservative:   0
Best Local Similarity:  99.64%          Mismatches:     2
Query Match:            99.55%          Indels:         0
DB:                     6               Gaps:           0

US-10-044-205A-2 (1-553) x AX357902 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
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Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
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Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
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Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
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Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 15
AX166511
LOCUS       AX166511                1662 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2 from Patent WO0138503.
ACCESSION   AX166511
VERSION     AX166511.1  GI:14546856
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
            Flanagan,P. and Clary,D.S.
  TITLE     Novel human protein kinases and protein kinase-like enzymes
  JOURNAL   Patent: WO 0138503-A 2 31-MAY-2001;
            Sugen, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              5.52e-249       Length:         1662
Score:                  2868.00         Matches:        550
Percent Similarity:     99.46%          Conservative:   0
Best Local Similarity:  99.46%          Mismatches:     3
Query Match:            99.27%          Indels:         0
DB:                     6               Gaps:           0

US-10-044-205A-2 (1-553) x AX166511 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
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Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
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Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
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Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGGGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAAGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
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Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
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Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
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Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
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Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

Search completed: August 13, 2004, 20:25:11
Job time : 4257 secs
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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:         August 13, 2004, 16:49:07 ; Search time 449 Seconds
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Title:          US-10-044-205A-2
Perfect score:  2889
Sequence:       1 MVDMGALDNLIANTAYLQAR..........NRPTGCEEGNSSKSGVCLLL 553

Scoring table:  BLOSUM62
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                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:      6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US10044205/runat_06082004_104321_23348/app_query.fasta_1.711
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES
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Result          Query
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   2     2883    99.8   1662  4  AAH78797           Aah78797 Human G-p
   3     2883    99.8   1662  6  ABQ86178           Abq86178 Novel hum
   4     2883    99.8   1662  6  AAD26466           Aad26466 Human kin
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   6     2883    99.8   1761  7  ABZ56943           Abz56943 Human gen
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  17   1284.5    44.5   2113  2  AAX90218           Aax90218 GRK4 poly
  18   1252.5    43.4   2511  2  AAV71032           Aav71032 Grk5-gree
  19   1252.5    43.4   2519  7  ACA03892           Aca03892 cDNA upre
  20.  1252.5    43.4   2529  2  AAV71024           Aav71024 Grk5-gree
  21   1252.5    43.4   2557  6  AAD36142           Aad36142 Human G p
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  30     1233    42.7   2541  9  ADB53307           Adb53307 Primary r
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  32   1226.5    42.5   2557  6  ABK49404           Abk49404 cDNA enco
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  34   1210.5    41.9   1879  2  AAX90221           Aax90221 GRK4 poly
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  37   1202.5    41.6   1996  5  AAS80696           Aas80696 DNA encod
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  41    984.5    34.1   1324  2  AAX90223           Aax90223 GRK4 poly
  42    852.5    29.5   1316  7  ABX74511           Abx74511 Human cDN
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  44    725.5    25.1   2362  8  ADB48363           Adb48363 Novel hum
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```
                              ALIGNMENTS

RESULT 1
ABS57375
ID   ABS57375 standard; cDNA; 2198 BP.
XX
AC   ABS57375;
XX
DT   04-FEB-2003  (first entry)
XX
DE   cDNA encoding human GPCR kinase (GPCRK) 69087.
XX
KW   Human; G protein coupled receptor kinase; GPCRK 69087;
KW   cellular proliferative disorder; differentiative disorder;
KW   haematopoietic neoplastic disorder; leukaemia; carcinoma; sarcoma;
KW   metastatic disorder; cytostatic; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             291. .1952
FT                   /*tag=  a
FT                   /product= "GPCRK 69087"
FT                   /note= "The coding sequence given as SEQ ID No:3 is
FT                   specifically claimed in Claim 1"
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PN   US2002123464-A1.
XX
PD   05-SEP-2002.
XX
PF   22-OCT-2001; 2001US-00044205.
XX
PR   19-OCT-2000; 2000US-0241884P.
PR   20-OCT-2000; 2000US-0241877P.
PR   23-OCT-2000; 2000US-0242428P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R,  Bandaru R;
XX
DR   WPI; 2003-066811/06.
DR   P-PSDB; ABG72173.
XX
PT   Novel isolated G protein coupled receptor kinase, 69087, nuclear
PT   signaling protein, 15821 or mitogen activated protein kinase phosphatase,
PT   15418, useful for treating cellular proliferative or differentiative
PT   disorders.
XX
PS   Claim 1; Fig 1; 98pp; English.
XX
CC   The present invention relates to the isolation of a novel human G protein
CC   coupled receptor (GPCR) kinase (GPCRK) designated 69087), a novel human
CC   nuclear signalling protein designated 15821, and a novel human mitogen-
CC   activated protein kinase (MAPK) phosphatase MAPKP designated 15418, and
CC   the polynucleotide sequences encoding them. The sequences of the
CC   invention are useful for treating and diagnosing disorders such as
CC   cellular proliferative and differentiative disorders (e.g. haematopoietic
CC   neoplastic disorders, leukaemia, carcinoma, sarcoma or metastatic
CC   disorders). They are also useful in screening assays, detection assays
CC   (e.g. chromosomal mapping, tissue typing, forensic biology), predictive
CC   medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical
CC   trials and pharmacogenomics), and in methods of treatment (e.g.
CC   therapeutic and prophylactic). The sequences may also be used to screen
CC   public databases to identify other family members or related sequences.
CC   The polypeptide sequences are useful as immunogens to generate antibodies
CC   that bind the polypeptides. The polynucleotide sequences are useful for
CC   mapping their respective genes on a chromosome, identifying gene regions
CC   associated with cellular proliferative or differentiative disorders, and
CC   in gene therapy. The present sequence encodes human GPCRK 69087
XX
SQ   Sequence 2198 BP; 558 A; 557 C; 607 G; 476 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.78e-282      Length:        2198
Score:                  2889.00        Matches:       553
Percent Similarity:     100.00%        Conservative:  0
Best Local Similarity:  100.00%        Mismatches:    0
Query Match:            100.00%        Indels:        0
DB:                     7              Gaps:          0

US-10-044-205A-2 (1-553) x ABS57375 (1-2198)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
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Db        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
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Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
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Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
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Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
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Db        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
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Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
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Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
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Db        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
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Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
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Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
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Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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Db       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1949

RESULT 2
AAH78797
ID   AAH78797 standard; cDNA; 1662 BP.
XX
AC   AAH78797;
XX
DT   08-MAR-2002  (first entry)
XX
DE   Human G-protein coupled receptor kinase 1 cDNA sequence.
XX
KW   G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
KW   drug screening; gene expression characterisation; NHP;
KW   novel human protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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PD   20-SEP-2001.
XX
PF   08-MAR-2001; 2001WO-US007500.
XX
PR   10-MAR-2000; 2000US-0188449P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Walke DW,  Wilganowski NL,  Turner CA;
XX
DR   WPI; 2001-570872/64.
DR   P-PSDB; AAG77815.
XX
PT   New polynucleotides encoding human proteins that share sequence
PT   similarity with animal kinases e.g. G-protein coupled receptor kinases,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Claim 1; Page 30; 34pp; English.
XX
CC   The present cDNA sequence encodes a human G-protein coupled receptor
CC   kinase (GRK), also designated NHP (novel human protein) in the
CC   specification, which is claimed in the invention. The invention comprises
CC   novel human nucleotide and protein sequences which have similarity to G-
CC   protein coupled receptor kinases. Oligonucleotides derived from the
CC   nucleotides of the invention are useful as hybridisation probes for
CC   screening libraries and assessing gene expression patterns. The
CC   nucleotides of the invention are also useful in drug screening and gene
CC   therapy for the modulation of GRK expression. The nucleotides of the
CC   invention can be used to genetically engineer host cells to express GRK
CC   products in vivo. The nucleotide sequences of the invention are also
CC   useful in addressable arrays for identifying and characterising the
CC   temporal and tissue specific expression of a gene and in microarrays to
CC   screen collections of genetic material from patients who have a
CC   particular medical condition. The proteins of the invention are useful
CC   for generating antibodies, as reagents in diagnostic assays, for
CC   identifying other cellular gene products related to GRK, and as reagents
CC   in assays for screening for compounds that are useful in the treatment of
CC   mental, biological or medical disorders/diseases
XX
SQ   Sequence 1662 BP; 420 A; 410 C; 479 G; 352 T; 0 U; 1 Other;

Alignment Scores:
Pred. No.:             7.61e-282      Length:        1662
Score:                 2883.00        Matches:       552
Percent Similarity:    99.82%         Conservative:  0
Best Local Similarity: 99.82%         Mismatches:    1
Query Match:           99.79%         Indels:        0
DB:                    4              Gaps:          0

US-10-044-205A-2 (1-553) x AAH78797 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
```

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 3
ABQ86178
ID   ABQ86178 standard; DNA; 1662 BP.
XX
AC   ABQ86178;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Novel human gene. SEQ ID 49.
XX
KW   Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian;
KW   nootropic; neuroprotective; immunosuppressive; haemostatic;
KW   antiinflammatory; cardiant; antiulcer; virucide; antithyroid;
KW   cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW   wound healing disorders; atherosclerosis; Parkinson's disease;
KW   Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW   inflammation; neoplastic disease; nervous system disorder;
KW   cardiovascular disorders; pancreatitis; respiratory disorder;
KW   hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW   developmental abnormality; gastrointestinal ulceration; neuropathy;
KW   haematological disease; metabolic disease; sperm dysfunction;
KW   thyroid disorder; hypothyroidism; brain damage; colitis;
KW   cone photo- transduction deficiency; neurological disease; stroke;
KW   angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
KW   trachea; thymus; lymph node; muscular system; obesity; anorexia;
KW   growth abnormality; precocious puberty; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200250105-A1.
XX
PD   27-JUN-2002.
XX
PF   17-DEC-2001; 2001WO-US049232.
XX
PR   19-DEC-2000; 2000US-0256710P.
PR   20-DEC-2000; 2000US-0257048P.
PR   09-JAN-2001; 2001US-0260482P.
PR   30-JAN-2001; 2001US-0264922P.
PR   06-FEB-2001; 2001US-0266797P.
PR   19-MAR-2001; 2001US-0276988P.
PR   04-APR-2001; 2001US-0281535P.
PR   08-MAY-2001; 2001US-0289622P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Agarwal P,  Birkeland M,  Cogswell JP,  Kabnick KF,  Lai Y;
PI   Martensen SA,  Rizvi SK,  Smith RF,  Strum JC,  Xie Q;
XX
DR   WPI; 2002-508784/54.
DR   P-PSDB; ABP61013.
XX
PT   Secreted proteins and polynucleotides useful as vaccines for preventing
PT   or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT   Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
XX
PS   Claim 2(a); Page 255-256; 335pp; English.
XX
CC   The invention relates to an isolated polypeptide with signal sequences
CC   which allow it to be secreted extracellularly or membrane associated. The
CC   activity of polypeptides of the invention may be described as,
CC   cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic,
CC   neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
CC   cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic,
CC   and metabolic. Polypeptides and polynucleotides of the invention are
CC   useful in the treatment, or as a vaccine in the prevention of, cancer,
CC   wound healing disorders, infection, atherosclerosis, Parkinson's disease
CC   and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
CC   inflammation, neoplastic diseases, nervous system related disorders and
CC   cardiovascular disorders, pancreatitis, respiratory disorder,
CC   hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC   developmental abnormality, gastrointestinal ulceration, neuropathy,
CC   haematological diseases, metabolic diseases, sperm dysfunction, thyroid
CC   disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC   transduction deficiency, neurological diseases, stroke, angiogenesis,
CC   ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC   trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC   growth abnormalities, and alleviation of precocious puberty. The
CC   sequences given in records ABQ86130-ABQ86184 represent novel human cDNA's
CC   of the invention
XX
SQ   Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

  Alignment Scores:
  Pred. No.:              7.61e-282      Length:          1662
  Score:                  2883.00        Matches:         552
  Percent Similarity:     99.82%         Conservative:    0
  Best Local Similarity:  99.82%         Mismatches:      1
  Query Match:            99.79%         Indels:          0
```

```
DB:                 6          Gaps:        0
US-10-044-205A-2 (1-553) x ABQ86178 (1-1662)
Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 4
AAD26466
ID   AAD26466 standard; cDNA; 1662 BP.
XX
AC   AAD26466;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human kinase PKIN-19 cDNA.
XX
KW   Human; kinase; PKIN-19; cancer; leukaemia; adenocarcinoma; osteoporosis;
KW   immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW   Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW   allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW   autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
KW   Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
KW   rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
KW   hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
KW   cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW   congestive heart failure; ischaemic heart disease; lung tumour; gout;
KW   fatty liver; Niemann-Pick's disease; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "Human PKIN-19 protein"
XX
PN   WO200196547-A2.
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XX
PD   20-DEC-2001.
XX
PF   14-JUN-2001; 2001WO-US019444.
XX
PR   15-JUN-2000; 2000US-0212073P.
PR   23-JUN-2000; 2000US-0213467P.
PR   30-JUN-2000; 2000US-0215651P.
PR   07-JUL-2000; 2000US-0216605P.
PR   13-JUL-2000; 2000US-0218372P.
PR   25-AUG-2000; 2000US-0228056P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yue H,  Lal P,  Bandman O,  Borowsky ML,  Au-Young J,  Lu Y;
PI   Gandhi AR,  Tribouley CM,  Walia NK,  Yao MG,  Lu DAM,  Greenwald SR;
PI   Ramkumar J,  Griffin JA,  Kearney L,  Burford N,  Nguyen DB,  Tang YT;
PI   Baughn MR,  He A,  Thornton M,  Hafalia A,  Patterson C,  Gururajan R;
PI   Lo TP,  Khan F,  Recipon SA,  Azimzai Y,  Policky JL,  Ding L;
PI   Grether M,  Elliott VS,  Thangavelu K,  Batra S,  Ison CH;
XX
DR   WPI; 2002-090207/12.
DR   P-PSDB; AAE16273.
XX
PT   New polypeptides, useful for diagnosing, treating or preventing disorders
PT   of growth and development, cardiovascular and lipid, and diseases such as
PT   cancer, comprise human kinase polypeptides.
XX
PS   Claim 5; Page 190; 197pp; English.
XX
CC   The invention relates to human kinase PKIN proteins and their
CC   corresponding cDNAs. A composition containing PKIN agonist is useful for
CC   treating a disease or condition associated with decreased expression of
CC   PKIN and a composition comprising PKIN antagonist is useful for treating
CC   a disease or condition associated with overexpression of PKIN. The
CC   disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
CC   myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder
CC   (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
CC   atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
CC   autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
CC   mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
CC   osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
CC   rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
CC   bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
CC   growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
CC   Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
CC   vascular disease (arteriovenous fistula, hypertension, vasculitis,
CC   aneurysms, congestive heart failure, angina pectoris, myocarditis,
CC   ischaemic heart disease, chronic bronchitis, lung tumours); lipid
CC   disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
CC   hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
CC   of a test compound and in gene therapy. The present sequence is human
CC   PKIN-19 cDNA
XX
SQ   Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.61e-282     Length:          1662
Score:                  2883.00       Matches:         552
Percent Similarity:     99.82%        Conservative:    0
Best Local Similarity:  99.82%        Mismatches:      1
Query Match:            99.79%        Indels:          0
DB:                     6             Gaps:            0

US-10-044-205A-2 (1-553) x AAD26466 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
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Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 5
AAD46350
ID   AAD46350 standard; cDNA; 1662 BP.
XX
AC   AAD46350;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Human cone opsin kinase (GRK7) cDNA.
XX
KW   Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
KW   GRK7; cone visual signalling; visual sensitivity; visual resolution;
KW   night blindness; colour blindness; Oguchi disease; Pineal gland activity;
KW   chronobiological desynchrony; depression; anxiety; memory loss; headache;
KW   mental fogginess; fatigue; jet lag; circadian rhythm; ophthalmological;
KW   gene therapy; antidepressant; analgesic; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1662
FT                   /*tag=  a
FT                   /product= "Human GRK7 protein"
XX
PN   WO200272541-A2.
XX
PD   19-SEP-2002.
XX
PF   07-MAR-2002; 2002WO-US007025.
XX
PR   07-MAR-2001; 2001US-0274006P.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Bird TA,  Spencer M,  Mosley BA;
XX
DR   WPI; 2002-723307/78.
DR   P-PSDB; AAE28952.
XX
PT   Identifying compounds that alter inhibition of cone opsin kinase
PT   polypeptide activity for treating a conditions related to cone visual
PT   signaling, comprises mixing a compound with a cone opsin kinase and with
PT   an inhibitory polypeptide.
XX
PS   Example 4; Page 45-46; 61pp; English.
XX
CC   The present invention relates to novel human cone opsin kinase (G-protein
CC   coupled receptor kinase 7; GRK7) and their corresponding polynucleotides.
CC   The invention further relates to a method of identifying compounds that
CC   alter the inhibition of GRK7 polypeptide activity which involves mixing a
CC   test compound with GRK7 protein and an inhibitory polypeptide and
CC   determining if the test compound alters the inhibition of GRK7 protein
CC   activity by the inhibitory polypeptide. GRK7 sequences are useful for
CC   treating conditions related to cone visual signalling (e.g., night
CC   blindness, colour blindness, difficulty with colour vision, visual
CC   sensitivity, visual resolution or in adapting to changes in light
CC   intensity, Oguchi disease or dominant congenital stationary night
CC   blindness), Pineal gland activity (e.g., chronobiological desynchrony,
CC   depression, anxiety, mental fogginess, memory loss, headaches, fatigue,
CC   or jet lag). Agonists of GRK7 polypeptide activity may be used to treat
CC   or ameliorate symptoms of a disease for which increased GRK7 polypeptide
CC   activity is beneficial, e.g., decreased colour sensitivity or other cone
CC   photoreceptor-mediated diseases. The GRK7 proteins are also useful in the
CC   preparation of a medicament for treating a condition or disease related
CC   to cone photoreceptor visual signaling or circadian rhythm, as molecular
CC   probes to screen for inherited defects in colour vision, circadian rhythm
CC   and vision resolution. They are also used as gene therapy tools for
CC   individuals with such disorders. The present sequence is human GRK7 cDNA
XX
SQ   Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                 7.61e-282    Length:          1662
Score:                     2883.00      Matches:         552
Percent Similarity:        99.82%       Conservative:    0
Best Local Similarity:     99.82%       Mismatches:      1
Query Match:               99.79%       Indels:          0
DB:                        6            Gaps:            0

US-10-044-205A-2 (1-553) x AAD46350 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy         181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy         201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy         221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy         241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy         261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy         281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy         301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy         341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy         361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy         381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy         401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy         421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy         441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy         461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy         481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy         501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy         521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy         541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
               |||||||||||||||||||||||||||||||||||||||
Db        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 6
ABZ56943
ID   ABZ56943 standard; DNA; 1761 BP.
XX
AC   ABZ56943;
XX
DT   04-APR-2003  (first entry)
XX
DE   Human gene sequence relative to the invention # SEQ ID 11.
XX
KW   Human; heart disease; cancer; omentopathy; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             26. .1687
FT                   /*tag=  a
XX
PN   WO2002103020-A1.
XX
PD   27-DEC-2002.
XX
PF   14-JUN-2002; 2002WO-JP005942.
XX
PR   15-JUN-2001; 2001JP-00182654.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Koyama N,  Tanida S,  Yamamoto K;
XX
DR   WPI; 2003-157045/15.
DR   P-PSDB; ABP60079.
XX
PT   Novel disease-associated gene of the RGS gene family and its product,
PT   applicable in diagnosis of and screening for drugs for heart diseases,
PT   cancers and omentopathy.
XX
PS   Example 3; Page 85-86; 96pp; Japanese.
XX
CC   The invention relates to a novel disease associated gene and its uses.
CC   The gene and its encoded protein are useful for diagnosis of and
CC   screening for drugs for heart diseases, cancers and omentopathy. The
CC   current sequence represents a human gene sequence relative to the
CC   invention
XX
SQ   Sequence 1761 BP; 441 A; 441 C; 504 G; 375 T; 0 U; 0 Other;

  Alignment Scores:
  Pred. No.:              8.25e-282     Length:          1761
  Score:                  2883.00       Matches:         552
  Percent Similarity:     99.82%        Conservative:    0
  Best Local Similarity:  99.82%        Mismatches:      1
  Query Match:            99.79%        Indels:          0
  DB:                     7             Gaps:            0

  US-10-044-205A-2 (1-553) x ABZ56943 (1-1761)

Qy           1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          26 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 85

Qy          21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          86 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 145

Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 205

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 265

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 325

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 385

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 445

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        446 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 505

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 565

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 625

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 685

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 745

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        746 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 805

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        806 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 865

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        866 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 925

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        926 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 985

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        986 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1045

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1046 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1105

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1106 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1165

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1166 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1225

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1226 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1285

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1286 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1345

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1346 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1405

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1406 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1465

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1466 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1525

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1526 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1585

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1586 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1645

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1646 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1684
```

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RESULT 7
ADC39221
ID   ADC39221 standard; cDNA; 1821 BP.
XX
AC   ADC39221;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Novel human NOVX polypeptide coding sequence SEQ ID NO: 165.
XX
KW   ds; gene; antidiabetic; cytostatic; immunomodulator; anorectic;
KW   antilipemic; nootropic; neuroprotective; immunostimulant;
KW   antiparkinsonian; anti-HIV; antiasthmatic; antiinflammatory; hypotensive;
KW   antiarteriosclerotic; hemostatic; osteopathic; gene therapy.; NOVX;
KW   diabetes; obesity; cancer; lymphoma; uterus cancer; prostate cancer;
KW   dyslipidemia; anorexia; wasting disorder; Alzheimer's disease;
KW   Parkinson's disorder; cachexia; cardiomyopathy; AIDS; asthma;
KW   Crohn's disease; multiple sclerosis; hypertension; atherosclerosis;
KW   hemophilia; graft-versus-host disease;
KW   Albright hereditary osteodystrophy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             73. .1732
FT                   /*tag=  a
XX
PN   WO2003010327-A2.
XX
PD   06-FEB-2003.
XX
PF   02-MAY-2002; 2002WO-US014199.
XX
PR   02-MAY-2001; 2001US-0288063P.
PR   03-MAY-2001; 2001US-0288395P.
PR   07-MAY-2001; 2001US-0289087P.
PR   09-MAY-2001; 2001US-0289817P.
PR   09-MAY-2001; 2001US-0289818P.
PR   11-MAY-2001; 2001US-0290194P.
PR   14-MAY-2001; 2001US-0290753P.
PR   15-MAY-2001; 2001US-0291181P.
PR   16-MAY-2001; 2001US-0291243P.
PR   18-MAY-2001; 2001US-0292001P.
PR   21-MAY-2001; 2001US-0292374P.
PR   22-MAY-2001; 2001US-0292587P.
PR   23-MAY-2001; 2001US-0293107P.
PR   25-MAY-2001; 2001US-0293747P.
PR   29-MAY-2001; 2001US-0294109P.
PR   29-MAY-2001; 2001US-0294110P.
PR   30-MAY-2001; 2001US-0294434P.
PR   31-MAY-2001; 2001US-0294827P.
PR   12-JUL-2001; 2001US-0304879P.
PR   31-JUL-2001; 2001US-0308901P.
PR   14-AUG-2001; 2001US-0312270P.
PR   17-AUG-2001; 2001US-0313416P.
PR   10-SEP-2001; 2001US-0318463P.
PR   27-SEP-2001; 2001US-0325683P.
PR   18-OCT-2001; 2001US-0330292P.
PR   28-NOV-2001; 2001US-0333873P.
PR   03-DEC-2001; 2001US-0336909P.
PR   03-DEC-2001; 2001US-0337552P.
PR   21-FEB-2002; 2002US-0359245P.
PR   01-MAY-2002; 2002US-00136826.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Miller CE,  Kekuda R,  Malyankar UM,  Li L,  Pena CEA,  Spytek KA;
PI   Gorman L,  Guo X,  Fernandes ER,  Smithson G,  Stone DJ,  Zerhusen BD;
PI   Patturajan M,  Anderson DW,  Mezes PS,  Peyman JA,  Macdougall JR;
PI   Padigaru M,  Rastelli L,  Shenoy SG,  Gerlach VL,  Shimkets RA,  Zhong M;
PI   Edinger SR,  Ellerman K;
XX
DR   WPI; 2003-239445/23.
DR   P-PSDB; ADC39222.
XX
PT   New NOVX polypeptides and polynucleotides, useful in gene therapy,
PT   particularly for treating or preventing a syndrome associated with a
PT   human disease e.g. diabetes, obesity, cancer, Alzheimer's disease,
PT   hypertension or hemophilia.
XX
PS   Claim 20; SEQ ID NO 165; 748pp; English.
XX
CC   The invention relates to new isolated NOVX polypeptides, the genes
CC   encoding them or sequences having at least 95% identity to the amino acid
CC   or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic,
CC   particularly in the manufacture of a medicament for treating a syndrome
CC   associated with a human disease, which includes a pathology associated
CC   with NOVX polypeptide. The NOVX polypeptide is particularly useful for
CC   treating, preventing or alleviating pathology associated with NOVX
CC   polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and
CC   polypeptide are especially useful for treating or preventing e.g.
CC   diabetes, obesity, cancers (e.g. lymphoma, uterus cancer or prostate
CC   cancer), dyslipidemias, anorexia, wasting disorders, Alzheimer's disease,
CC   Parkinson's disorder, cachexia, cardiomyopathy, AIDS, asthma, Crohn's
CC   disease, multiple sclerosis, hypertension, atherosclerosis, hemophilia,
CC   graft-versus-host disease or Albright hereditary osteodystrophy. The DNA
CC   encoding the protein is useful in gene therapy for treating the above
CC   conditions. These are also useful in developing powerful assay system for
CC   functional analysis of various human disorders, as well as in diagnostic
CC   applications. This sequence represents one of the NOVX genes of the
CC   invention.
XX
SQ   Sequence 1821 BP; 453 A; 459 C; 524 G; 385 T; 0 U; 0 Other;

  Alignment Scores:
  Pred. No.:                8.65e-282     Length:         1821
  Score:                    2883.00       Matches:        552
  Percent Similarity:       99.82%        Conservative:   0
  Best Local Similarity:    99.82%        Mismatches:     1
  Query Match:              99.79%        Indels:         0
  DB:                       9             Gaps:           0

US-10-044-205A-2 (1-553) x ADC39221 (1-1821)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 132

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 192

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 252

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 312

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 372

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 432

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 492

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        493 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 552

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        553 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 612

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 672

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 732

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        733 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 792

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        793 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 852

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        853 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 912

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        913 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 972

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        973 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1032

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1033 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1092

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1093 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1152

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1153 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1212
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Qy         381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1213 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1272

Qy         401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1273 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1332

Qy         421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1333 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1392

Qy         441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1393 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1452

Qy         461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1453 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1512

Qy         481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1513 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1572

Qy         501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1573 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1632

Qy         521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1633 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1692

Qy         541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
               |||||||||||||||||||||||||||||||||||||||
Db        1693 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1731

RESULT 8
AAH78799
ID   AAH78799 standard; cDNA; 2249 BP.
XX
AC   AAH78799;
XX
DT   08-MAR-2002  (first entry)
XX
DE   Human G-protein coupled receptor kinase 3 cDNA sequence.
XX
KW   G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
KW   drug screening; gene expression characterisation; NHP;
KW   novel human protein.
XX
OS   Homo sapiens.
XX
PN   WO200168869-A2.
XX
PD   20-SEP-2001.
XX
PF   08-MAR-2001; 2001WO-US007500.
XX
PR   10-MAR-2000; 2000US-0188449P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Walke DW,  Wilganowski NL,  Turner CA;
XX
DR   WPI; 2001-570872/64.
XX
PT   New polynucleotides encoding human proteins that share sequence
PT   similarity with animal kinases e.g. G-protein coupled receptor kinases,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Disclosure; Page 33-34; 34pp; English.
XX
CC   The present cDNA sequence encodes a human G-protein coupled receptor
CC   kinase (GRK), also designated NHP (novel human protein) in the
CC   specification, which is shown in the sequence listing. The invention
CC   comprises novel human nucleotide and protein sequences which have
CC   similarity to G-protein coupled receptor kinases. Oligonucleotides
CC   derived from the nucleotides of the invention are useful as hybridisation
CC   probes for screening libraries and assessing gene expression patterns.
CC   The nucleotides of the invention are also useful in drug screening and
CC   gene therapy for the modulation of GRK expression. The nucleotides of the
CC   invention can be used to genetically engineer host cells to express GRK
CC   products in vivo. The nucleotide sequences of the invention are also
CC   useful in addressable arrays for identifying and characterising the
CC   temporal and tissue specific expression of a gene and in microarrays to
CC   screen collections of genetic material from patients who have a
CC   particular medical condition. The proteins of the invention are useful
CC   for generating antibodies, as reagents in diagnostic assays, for
CC   identifying other cellular gene products related to GRK, and as reagents
CC   in assays for screening for compounds that are useful in the treatment of
CC   mental, biological or medical disorders/diseases
XX
SQ   Sequence 2249 BP; 582 A; 577 C; 608 G; 482 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.16e-281     Length:         2249
Score:                  2883.00       Matches:        552
Percent Similarity:     99.82%        Conservative:   0
Best Local Similarity:  99.82%        Mismatches:     1
Query Match:            99.79%        Indels:         0
DB:                     4             Gaps:           0

US-10-044-205A-2 (1-553) x AAH78799 (1-2249)

Qy           1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         354 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 413

Qy          21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         414 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 473

Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 533

Qy          61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         534 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 593

Qy          81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         594 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 653

Qy         101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         654 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 713

Qy         121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         714 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 773

Qy         141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
               |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db         774 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 833

Qy         161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         834 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 893

Qy         181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         894 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGAAAGGT 953

Qy         201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          954 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 1013

Qy          221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Db         1014 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1073

Qy          241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Db         1074 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1133

Qy          261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1134 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1193

Qy          281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1194 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1253

Qy          301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1254 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1313

Qy          321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1373

Qy          341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1374 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1433

Qy          361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Db         1434 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1493

Qy          381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
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Db         1494 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1553

Qy          401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
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Db         1554 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1613

Qy          421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy          441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
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Db         1674 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1733

Qy          461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1734 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1793

Qy          481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1794 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1853

Qy          501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1854 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1913

Qy          521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1914 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973

Qy          541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
                |||||||||||||||||||||||||||||||||||||||
Db         1974 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 2012

RESULT 9
ACC44827
ID   ACC44827 standard; cDNA; 3186 BP.
XX
AC   ACC44827;
XX
DT   04-JUN-2003  (first entry)
XX
DE   Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:4.
XX
KW   Human; G protein coupled receptor kinase; GRK; cytostatic; antidiabetic;
KW   neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiant;
KW   vasotropic; antiasthmatic; gene therapy; cancer; diabetes; CNS disorder;
KW   central nervous system disorder; cardiovascular disorder; asthma; COPD;
KW   chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;
KW   Alzheimer's disease; Parkinson's disease; congestive heart failure;
KW   myocardial infarction; ischaemic disease; hypertensive vascular disease;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             85. .1746
FT                   /*tag=  a
FT                   /product= "G protein-coupled receptor kinase (GRK)"
XX
PN   WO2003018815-A2.
XX
PD   06-MAR-2003.
XX
PF   19-AUG-2002; 2002WO-EP009235.
XX
PR   21-AUG-2001; 2001US-0313464P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; 2003-278669/27.
DR   P-PSDB; ABP96709.
XX
PT   New G-protein coupled receptor kinase polypeptides and polynucleotides,
PT   useful in identifying modulators of the enzyme for treating cancer,
PT   diabetes, a central nervous system disorder, a cardiovascular disorder or
PT   asthma.
XX
PS   Claim 1; Fig 11; 129pp; English.
XX
CC   The present sequence encodes a human G protein-coupled receptor kinase
CC   (GRK) protein (I). (I) has cytostatic, antidiabetic, neuroprotective,
CC   nootropic, cardiovascular, anti-Parkinsonian, cardiant, vasotropic and
CC   antiasthmatic activities, and can be used in gene therapy. (I) can be
CC   regulated to treat cancer, diabetes, a central nervous system (CNS)
CC   disorder (e.g. anxiety or mood disorders, Alzheimer's disease and
CC   Parkinson's disease), cardiovascular disorders (e.g. congestive heart
CC   failure, myocardial infarction, ischaemic diseases of the heart or
CC   hypertensive vascular disease), asthma and chronic obstructive pulmonary
CC   disorder (COPD). GRK molecules are useful in screening for agents that
CC   regulate or decease the activity of a GRK. GRK sequences may also be used
CC   for detecting diseases and abnormalities or susceptibility to diseases
CC   and abnormalities related to the presence of mutations in the nucleic
CC   acid sequences that encode the GRK enzyme
XX
SQ   Sequence 3186 BP; 857 A; 737 C; 784 G; 808 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:               1.89e-281       Length:          3186
Score:                   2883.00         Matches:         552
Percent Similarity:      99.82%          Conservative:    0
Best Local Similarity:   99.82%          Mismatches:      1
Query Match:             99.79%          Indels:          0
DB:                      7               Gaps:            0

US-10-044-205A-2 (1-553) x ACC44827 (1-3186)
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Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
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Db         85 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 144

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 204

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 264

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 324

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 384

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 444

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 504

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        505 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 564

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 624

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 684

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 744

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 804

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 864

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
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Db        865 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 924

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 984

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
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Db        985 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1044

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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Db       1045 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1104

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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Db       1105 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1164

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
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Db       1165 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1224

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
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Db       1225 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1284

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
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Db       1285 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1344

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1345 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1404

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1405 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1464

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
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Db       1465 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1524

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
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Db       1525 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1584

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
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Db       1585 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1644

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
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Db       1645 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1704

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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Db       1705 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1743

RESULT 10
AAD28071
ID   AAD28071 standard; cDNA; 1662 BP.
XX
AC   AAD28071;
XX
DT   22-APR-2002  (first entry)
XX
DE   Human kinase cDNA.
XX
KW   Human; kinase; G-protein coupled receptor kinase; tissue differentiation;
KW   chromosome 3; therapeutic; immune response; drug screening; enzyme; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "Human kinase protein"
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PN   WO200192496-A2.
XX
PD   06-DEC-2001.
XX
PF   31-MAY-2001; 2001WO-US017510.
XX
PR   01-JUN-2000; 2000US-0208331P.
PR   18-DEC-2000; 2000US-00738894.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Guegler K,  Di Francesco V,  Beasley EM;
XX
DR   WPI; 2002-130533/17.
DR   P-PSDB; AAE17136.
XX
PT   New isolated human kinase proteins and nucleic acids, useful as a major
PT   target for drug action and development, particularly for screening
PT   modulators of the kinase peptides.
XX
PS   Claim 4; Fig 1; 87pp; English.
XX
CC   The invention relates to human kinase proteins that are related to G-
CC   protein coupled receptor kinase subfamily. Human kinase gene is located
CC   on chromosome 3. The kinase peptide and nucleic acid are useful in the
CC   development of human therapeutic and diagnostic compositions. The peptide
CC   is useful as a major target for drug action and development, and is
CC   valuable to the field of pharmaceutical development to identify and
CC   characterise modulators of the kinase. The proteins may also be used to
CC   raise antibodies or to elicit an immune response, as a reagent in assays
CC   designed to quantitatively determine levels of the protein in biological
CC   fluids and as markers for tissues in which the corresponding protein is
CC   preferentially expressed (either constitutively or at a particular stage
CC   of tissue differentiation or development or in a disease state). The
CC   kinase proteins are also useful for providing a target for diagnosing a
CC   disease or predisposition to disease mediated by the peptide. The nucleic
CC   acid molecules are useful for probes, primers, chemical intermediates and
CC   in biological assays. The nucleic acids are also useful in making vectors
CC   containing the gene regulatory regions of the nucleic acid molecules and
CC   for drug screening to identify compounds that modulate kinase nucleic
CC   acid expression. The present sequence is human kinase cDNA expressed in
CC   skins, germinal center B cells, colon, kidney and lung
XX
SQ   Sequence 1662 BP; 419 A; 411 C; 480 G; 352 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              3.9e-281      Length:          1662
Score:                  2876.00       Matches:         551
Percent Similarity:     99.64%        Conservative:    0
Best Local Similarity:  99.64%        Mismatches:      2
Query Match:            99.55%        Indels:          0
DB:                     6             Gaps:            0

US-10-044-205A-2 (1-553) x AAD28071 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
```

```
Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
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                 ||||||||||||||||||||
Db        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy         541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
               |||||||||||||
Db        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 11
AAS06702
ID   AAS06702 standard; cDNA; 1662 BP.
XX
AC   AAS06702;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Polynucleotide sequence encoding human protein kinase #2.
XX
KW   Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW   metabolic disorder; immune related disease; neurological disorder;
KW   neurodegenerative disorder; inflammatory disorder; infectious disease;
KW   reproductive disorder; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138503-A2.
XX
PD   31-MAY-2001.
XX
PF   22-NOV-2000; 2000WO-US032085.
XX
PR   24-NOV-1999;   99US-0167482P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD,  Whyte D,  Manning G,  Sudarsanam S,  Martinez R;
PI   Flanagan P,  Clary D;
XX
DR   WPI; 2001-343950/36.
DR   P-PSDB; AAU03502.
XX
PT   Nucleic acids encoding human kinase polypeptides, useful for preventing
PT   diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT   neuronal-associated diseases, and microbial infections.
XX
PS   Example 1; Fig 1; 433pp; English.
XX
CC   AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
CC   protein kinases have been identified as members of the tyrosine or
CC   serine/threonine kinase (PTK and STK) families. The polynucleotides
CC   encoding protein kinases and the polypeptides may be used in the
CC   prevention, diagnosis and treatment of diseases associated with
CC   inappropriate kinase expression. For example, they may be used to treat
CC   cancers (especially cancers of haematopoietic origin), cardiovascular
CC   disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC   immune related diseases (e.g. rheumatoid arthritis), neurological
CC   disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC   Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC   disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC   Additionally, polynucleotides encoding protein kinases may be used for
CC   gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC   polypeptides may be used as antigens in the production of antibodies
CC   against the protein kinases and in assays to identify modulators of
CC   protein kinase expression and activity
XX
SQ   Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.52e-280     Length:         1662
Score:                  2868.00       Matches:        550
Percent Similarity:     99.46%        Conservative:   0
Best Local Similarity:  99.46%        Mismatches:     3
Query Match:            99.27%        Indels:         0
DB:                     4             Gaps:           0

US-10-044-205A-2 (1-553) x AAS06702 (1-1662)

Qy           1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
               ||||||||||||||||||||
Db           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy          21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
               ||||||||||||||||||||
Db          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
               ||||||||||||||||||||
Db         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy          61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
               ||||||||||||||||||||
Db         181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy          81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
               ||||||||||||||||||||
Db         241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy         101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
               ||||||||||||||||||||
Db         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy         121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
               ||||||||||||||||||||
Db         361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy         141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
               ||||||||| ||||||||||
Db         421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy         161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
               ||||||||||||||||||||
Db         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy         181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
               ||||||||||||||||||||
Db         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy         201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
               ||||||||||||||||||||
Db         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy         221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
               ||||||||||||||||||||
Db         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy         241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
               ||||||||||||||||||||
Db         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy         261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
               ||||||||||||||||||||
Db         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy         281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
               ||||||||||||||||||||
Db         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy         301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
               ||||||||||||||||||||
Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
               |||  |||||||||||||||
Db         961 AATGGGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy         341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
               ||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||   
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAAGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 12
ACC44826
ID   ACC44826 standard; cDNA; 1662 BP.
XX
AC   ACC44826;
XX
DT   04-JUN-2003  (first entry)
XX
DE   Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:1.
XX
KW   Human; G protein coupled receptor kinase; GRK; cytostatic; antidiabetic;
KW   neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiant;
KW   vasotropic; antiasthmatic; gene therapy; cancer; diabetes; CNS disorder;
KW   central nervous system disorder; cardiovascular disorder; asthma; COPD;
KW   chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;
KW   Alzheimer's disease; Parkinson's disease; congestive heart failure;
KW   myocardial infarction; ischaemic disease; hypertensive vascular disease;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "G protein-coupled receptor kinase (GRK)"
XX
PN   WO2003018815-A2.
XX
PD   06-MAR-2003.
XX
PF   19-AUG-2002; 2002WO-EP009235.
XX
PR   21-AUG-2001; 2001US-0313464P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; 2003-278669/27.
DR   P-PSDB; ABP96707.
XX
PT   New G-protein coupled receptor kinase polypeptides and polynucleotides,
PT   useful in identifying modulators of the enzyme for treating cancer,
PT   diabetes, a central nervous system disorder, a cardiovascular disorder or
PT   asthma.
XX
PS   Claim 1; Fig 1; 129pp; English.
XX
CC   The present sequence encodes a human G protein-coupled receptor kinase
CC   (GRK) protein (I). (I) has cytostatic, antidiabetic, neuroprotective,
CC   nootropic, cardiovascular, anti-Parkinsonian, cardiant, vasotropic and
CC   antiasthmatic activities, and can be used in gene therapy. (I) can be
CC   regulated to treat cancer, diabetes, a central nervous system (CNS)
CC   disorder (e.g. anxiety or mood disorders, Alzheimer's disease and
CC   Parkinson's disease), cardiovascular disorders (e.g. congestive heart
CC   failure, myocardial infarction, ischaemic diseases of the heart or
CC   hypertensive vascular disease), asthma and chronic obstructive pulmonary
CC   disorder (COPD). GRK molecules are useful in screening for agents that
CC   regulate or decease the activity of a GRK. GRK sequences may also be used
CC   for detecting diseases and abnormalities or susceptibility to diseases
CC   and abnormalities related to the presence of mutations in the nucleic
CC   acid sequences that encode the GRK enzyme
XX
SQ   Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.52e-280       Length:          1662
Score:                  2868.00         Matches:         550
Percent Similarity:     99.46%          Conservative:    0
Best Local Similarity:  99.46%          Mismatches:      3
Query Match:            99.27%          Indels:          0
DB:                     7               Gaps:            0

US-10-044-205A-2 (1-553) x ACC44826 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
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            |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db     421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy     161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy     181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy     201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy     221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy     241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy     261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy     281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy     301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy     321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
            |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     961 AATGGGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy     341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy     361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy     381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy     401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy     421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAAGA 1320

Qy     441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy     461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy     481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy     501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy     521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy     541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
            |||||||||||||||||||||||||||||||||||||||
Db    1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 13
AAD46351
ID   AAD46351 standard; cDNA; 1486 BP.
XX
AC   AAD46351;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Human cone opsin kinase (GRK7) OK6 splice variant cDNA.
XX
KW   Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
KW   GRK7; cone visual signalling; visual sensitivity; visual resolution;
KW   night blindness; colour blindness; Oguchi disease; Pineal gland activity;
KW   chronobiological desynchrony; depression; anxiety; memory loss; headache;
KW   mental fogginess; fatigue; jet lag; circadian rhythm; ophthalmological;
KW   gene therapy; antidepressant; analgesic; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1062
FT                   /*tag=  a
FT                   /product= "Human GRK7 OK6 splice variant protein"
XX
PN   WO200272541-A2.
XX
PD   19-SEP-2002.
XX
PF   07-MAR-2002; 2002WO-US007025.
XX
PR   07-MAR-2001; 2001US-0274006P.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Bird TA,  Spencer M,  Mosley BA;
XX
DR   WPI; 2002-723307/78.
DR   P-PSDB; AAE28953.
XX
PT   Identifying compounds that alter inhibition of cone opsin kinase
PT   polypeptide activity for treating a conditions related to cone visual
PT   signaling, comprises mixing a compound with a cone opsin kinase and with
PT   an inhibitory polypeptide.
XX
PS   Example 4; Page 48-49; 61pp; English.
XX
CC   The present invention relates to novel human cone opsin kinase (G-protein
CC   coupled receptor kinase 7; GRK7) and their corresponding polynucleotides.
CC   The invention further relates to a method of identifying compounds that
CC   alter the inhibition of GRK7 polypeptide activity which involves mixing a
CC   test compound with GRK7 protein and an inhibitory polypeptide and
CC   determining if the test compound alters the inhibition of GRK7 protein
CC   activity by the inhibitory polypeptide. GRk7 sequences are useful for
CC   treating conditions related to cone visual signalling (e.g., night
CC   blindness, colour blindness, difficulty with colour vision, visual
CC   sensitivity, visual resolution or in adapting to changes in light
CC   intensity, Oguchi disease or dominant congenital stationary night
CC   blindness), Pineal gland activity (e.g., chronobiological desynchrony,
CC   depression, anxiety, mental fogginess, memory loss, headaches, fatigue,
CC   or jet lag). Agonists of GRK7 polypeptide activity may be used to treat
CC   or ameliorate symptoms of a disease for which increased GRK7 polypeptide
CC   activity is beneficial, e.g., decreased colour sensitivity or other cone
CC   photoreceptor-mediated diseases. The GRK7 proteins are also useful in the
CC   preparation of a medicament for treating a condition or disease related
CC   to cone photoreceptor visual signaling or circadian rhythm, as molecular
CC   probes to screen for inherited defects in colour vision, circadian rhythm
CC   and vision resolution. They are also used as gene therapy tools for
CC   individuals with such disorders. The present sequence is human GRK7 OK6
CC   splice variant cDNA
XX
SQ   Sequence 1486 BP; 353 A; 387 C; 434 G; 312 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.74e-225       Length:        1486
Score:                  2326.00         Matches:       460
Percent Similarity:     83.03%          Conservative:  0
Best Local Similarity:  83.03%          Mismatches:    1
Query Match:            80.51%          Indels:        93
DB:                     6               Gaps:          1

US-10-044-205A-2 (1-553) x AAD46351 (1-1486)

Qy           1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy          21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy          61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy          81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy         101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy         121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy         141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
               |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db         421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy         161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy         181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy         201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy         221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy         241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy         261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy         281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy         301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy         341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
               |||||||||||||||||||||||||||
Db        1021 ATGAAGGGTGGCAAGCCCATCACCCAG--------------------------------- 1047

Qy         361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380

Db        1047 ------------------------------------------------------------ 1047

Qy         381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400

Db        1047 ------------------------------------------------------------ 1047

Qy         401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420

Db        1047 ------------------------------------------------------------ 1047

Qy         421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440

Db        1047 ------------------------------------------------------------ 1047

Qy         441 SerArg-GluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePr 460
                  ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1048 ---AGGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCC 1104

Qy         460 oArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAl 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1105 TCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGC 1164

Qy         480 aLysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLy 500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1165 CAAAGACATCGCCGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAA 1224

Qy         500 sAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGl 520
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1225 AGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGA 1284

Qy         520 uIleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGl 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1285 AATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGA 1344

Qy         540 uGluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
               ||||||||||||||||||||||||||||||||||||||||
Db        1345 GGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1384

RESULT 14
ABZ56934
ID   ABZ56934 standard; DNA; 1191 BP.
XX
AC   ABZ56934;
XX
DT   04-APR-2003  (first entry)
XX
DE   Human RGSNo9 encoding DNA # SEQ ID 2.
XX
KW   Human; RGSNo9; heart disease; cancer; omentopathy; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key                 Location/Qualifiers
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FT   CDS             1. .1191
FT                   /*tag=  a
FT                   /product= "RGSNo9"
XX
PN   WO2002103020-A1.
XX
PD   27-DEC-2002.
XX
PF   14-JUN-2002; 2002WO-JP005942.
XX
PR   15-JUN-2001; 2001JP-00182654.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Koyama N,  Tanida S,  Yamamoto K;
XX
DR   WPI; 2003-157045/15.
DR   P-PSDB; ABP60078.
XX
PT   Novel disease-associated gene of the RGS gene family and its product,
PT   applicable in diagnosis of and screening for drugs for heart diseases,
PT   cancers and omentopathy.
XX
PS   Claim 6; Page 81-82; 96pp; Japanese.
XX
CC   The invention relates to a novel disease associated gene and its uses.
CC   The gene and its encoded protein are useful for diagnosis of and
CC   screening for drugs for heart diseases, cancers and omentopathy. The
CC   current sequence represents the human RGSNo9 encoding DNA sequence
XX
SQ   Sequence 1191 BP; 274 A; 320 C; 363 G; 234 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.8e-198      Length:        1191
Score:                  2058.00       Matches:       396
Percent Similarity:     99.75%        Conservative:  0
Best Local Similarity:  99.75%        Mismatches:    1
Query Match:            71.24%        Indels:        0
DB:                     7             Gaps:          0

US-10-044-205A-2 (1-553) x ABZ56934 (1-1191)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLys 397
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAG 1191

RESULT 15
AAH78798
ID   AAH78798 standard; cDNA; 1062 BP.
XX
AC   AAH78798;
XX
DT   08-MAR-2002  (first entry)
XX
DE   Human G-protein coupled receptor kinase 2 cDNA sequence.
XX
KW   G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
KW   drug screening; gene expression characterisation; NHP;
KW   novel human protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1062
FT                   /*tag=  a
FT                   /product= "G-protein coupled receptor kinase 2"
XX
PN   WO200168869-A2.
XX
PD   20-SEP-2001.
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XX
PF   08-MAR-2001; 2001WO-US007500.
XX
PR   10-MAR-2000; 2000US-0188449P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Walke DW,  Wilganowski NL,  Turner CA;
XX
DR   WPI; 2001-570872/64.
DR   P-PSDB; AAG77816.
XX
PT   New polynucleotides encoding human proteins that share sequence
PT   similarity with animal kinases e.g. G-protein coupled receptor kinases,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Claim 4; Page 32; 34pp; English.
XX
CC   The present cDNA sequence encodes a human G-protein coupled receptor
CC   kinase (GRK), also designated NHP (novel human protein) in the
CC   specification, which is claimed in the invention. The invention comprises
CC   novel human nucleotide and protein sequences which have similarity to G-
CC   protein coupled receptor kinases. Oligonucleotides derived from the
CC   nucleotides of the invention are useful as hybridisation probes for
CC   screening libraries and assessing gene expression patterns. The
CC   nucleotides of the invention are also useful in drug screening and gene
CC   therapy for the modulation of GRK expression. The nucleotides of the
CC   invention can be used to genetically engineer host cells to express GRK
CC   products in vivo. The nucleotide sequences of the invention are also
CC   useful in addressable arrays for identifying and characterising the
CC   temporal and tissue specific expression of a gene and in microarrays to
CC   screen collections of genetic material from patients who have a
CC   particular medical condition. The proteins of the invention are useful
CC   for generating antibodies, as reagents in diagnostic assays, for
CC   identifying other cellular gene products related to GRK, and as reagents
CC   in assays for screening for compounds that are useful in the treatment of
CC   mental, biological or medical disorders/diseases
XX
SQ   Sequence 1062 BP; 237 A; 296 C; 330 G; 199 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.67e-172     Length:         1062
Score:                  1801.00       Matches:        349
Percent Similarity:     99.71%        Conservative:   0
Best Local Similarity:  99.71%        Mismatches:     1
Query Match:            62.34%        Indels:         0
DB:                     4             Gaps:           0

US-10-044-205A-2 (1-553) x AAH78798 (1-1062)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArg 350
              ||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1050

Search completed: August 13, 2004, 19:14:24
Job time : 481 secs
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                     GenCore version 5.1.6
              Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:          August 13, 2004, 18:42:11 ; Search time 2705 Seconds
                                              (without alignments)
                                              6104.912 Million cell updates/sec

Title:           US-10-044-205A-2
Perfect score:   2889
Sequence:        1 MVDMGALDNLIANTAYLQAR..........NRPTGCEEGNSSKSGVCLLL 553

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters:        55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10044205/runat_06082004_104322_23369/app_query.fasta_1.711
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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       EST:*
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                 14:  gb_est5:*
                 15:  em_estfun:*
                 16:  em_estom:*
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                 18:  em_gss_inv:*
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                 20:  em_gss_vrt:*
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                 22:  em_gss_mam:*
                 23:  em_gss_mus:*
                 24:  em_gss_pro:*
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                 29:  gb_gss2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                                   SUMMARIES
                   %
Result             Query
   No.   Score     Match Length DB  ID                          Description
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    1     1262     43.7   2329  11  BC027597                 BC027597 Homo sapi
    2   1219.5     42.2   2989  11  BC057206                 BC057206 Mus muscu
    3   1218.5     42.2   2978  11  AK051405                 AK051405 Mus muscu
    4    955.5     33.1   1721  29  AY406080                 AY406080 Homo sapi
    5    940.5     32.6   1721  29  AY406082                 AY406082 Mus muscu
c   6    883.5     30.6   1201  13  BX404586                 BX404586 BX404586
    7    826.5     28.6    968  13  BQ066445                 BQ066445 AGENCOURT
    8    822.5     28.5    998  13  BQ057613                 BQ057613 AGENCOURT
    9    813.5     28.2   1017  13  BQ061150                 BQ061150 AGENCOURT
   10    803.5     27.8   1019  13  BQ061148                 BQ061148 AGENCOURT
   11    796.5     27.6   1028  13  BQ063841                 BQ063841 AGENCOURT
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c  14    791.5     27.4    917  13  BX392018                 BX392018 BX392018
   15      787     27.2    838  13  BX849055                 BX849055 BX849055
c  16    782.5     27.1    769  13  BW013848                 BW013848 BW013848
   17      780     27.0    995  13  BQ056240                 BQ056240 AGENCOURT
   18    767.5     26.6    903  13  BU146436                 BU146436 AGENCOURT
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   20      761     26.3    988  13  BQ066396                 BQ066396 AGENCOURT
c  21      752     26.0    810  13  BW085647                 BW085647 BW085647
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   23    740.5     25.6    990  13  BQ071614                 BQ071614 AGENCOURT
c  24    737.5     25.5    724  13  BW014695                 BW014695 BW014695
   25    737.5     25.5    857  13  BU527897                 BU527897 AGENCOURT
   26    737.5     25.5   1002  13  BQ065277                 BQ065277 AGENCOURT
   27      737     25.5    937  12  BG477593                 BG477593 602522431
   28    731.5     25.3    660  13  BQ520195                 BQ520195 NISC_nl03
   29    731.5     25.3   1622  29  AY406081                 AY406081 Pan trogl
   30      729     25.2    962  13  BQ061253                 BQ061253 AGENCOURT
c  31    728.5     25.2    718  13  BW014526                 BW014526 BW014526
   32    728.5     25.2   1796   8  BC021221                 Bc021221 Homo sapi
   33    720.5     24.9    765   9  AJ442768                 AJ442768 AJ442768
c  34    717.5     24.8    815   9  AI934968                 AI934968 wd17a07.x
   35    712.5     24.7    984  13  BQ055527                 BQ055527 AGENCOURT
   36    702.5     24.3   1057  13  BQ071329                 BQ071329 AGENCOURT
c  37    700.5     24.2    696  10  BE677821                 BE677821 7f63e10.x
   38      700     24.2    906  14  CB195708                 CB195708 AGENCOURT
   39      699     24.2    892  14  CB195631                 CB195631 AGENCOURT
   40    697.5     24.1   1034  10  BF568334                 BF568334 602184519
   41    696.5     24.1   1067  12  BM927442                 BM927442 AGENCOURT
   42    692.5     24.0    800  14  CA463876                 CA463876 AGENCOURT
   43    690.5     23.9    726  14  CF520008                 CF520008 AGENCOURT
   44      685     23.7   1095  13  BQ058855                 BQ058855 AGENCOURT
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                                  ALIGNMENTS

RESULT 1
BC027597
LOCUS       BC027597                2329 bp    mRNA    linear   HTC 01-MAY-2002
DEFINITION  Homo sapiens, Similar to G protein-coupled receptor kinase 2-like
            (Drosophila), clone IMAGE:4830673, mRNA.
ACCESSION   BC027597
VERSION     BC027597.1  GI:20379554
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2329)
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AUTHORS     Strausberg,R.
TITLE       Direct Submission
JOURNAL     Submitted (08-APR-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK      NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) &  Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 34 Row: i Column: 14
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4885346
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4830673"
                     /tissue_type="Testis"
                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript"
ORIGIN

Alignment Scores:
Pred. No.:              7.86e-117     Length:          2329
Score:                  1262.00       Matches:         255
Percent Similarity:     65.43%        Conservative:    97
Best Local Similarity:  47.40%        Mismatches:      161
Query Match:            43.68%        Indels:          25
DB:                     11            Gaps:            9

US-10-044-205A-2 (1-553) x BC027597 (1-2329)

Qy          7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSer---AspCys 25
              |||:::|||::::::||||||:::      |||:::||||||:::
Db        463 CTCGAGAACATCGTGGCCAACTCGCTGCTGCTGAAAGCGCGTCAAGGAGGATATGGCAAA 522

Qy         26 AspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
                 |||         ::::::   :::      |||   ||||||   :::      |||
Db        523 AAAAGTGGTCGTAGTAAAAAATGGAAGGAGATACTGACACTGCCTCCTGTCAGCCAGTGC 582

Qy         46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
              :::|||||||||      :::      ::::::   |||||||||::::::|||||||||
Db        583 AGTGAGCTTAGACATTCCATTGAAAAGGATTATAGCAGTCTTTGTGACAAGCAACCGATA 642

Qy         66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
              ||||||||||||||||||   |||      |||   ||||||   ::::::
Db        643 GGAAGACGTCTCTTCAGGCAGTTCTGTGATACCAAACCCACTCTAAAGAGGCACATTGAA 702

Qy         86 PheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyProThrLysAsp------ 103
              ||||||:::   |||      :::|||:::|||::::::            |||
Db        703 TTCTTGGATGCAGTGGCAGAATATGAAGTTGCCGATGATGAGGACCGAAGTGATTGTGGA 762

Qy        104 ---SerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGlyAsnPro 122
                 |||   |||                        :::||||||   |||      |||
Db        763 CTGTCAATCTTAGATAGATTCTTCAATGATAAGTTGGCAGCCCCTTTACCAGAAATACCT 822

Qy        123 GlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGluGluGlu 142
                                   |||   |||:::|||:::            ||||||
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Db        823 CCAGAT---------------GTTGTGACAGAATGTAGATTGGGACTGAAGGAGGAGAAC 867

Qy        143 ArgValAlaAlaValThrLeuArgLysAla------------------GluAlaMetAla 156
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Db        868 ---------------CCTTCCAAAAAAGCCTTTGAGGAATGTACTAGAGTTGCCCATAAC 912

Qy        157 PheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeu 176
              :::|||:::   :::||||||:::::::::      |||:::::::::   :::||||||
Db        913 TACCTAAGAGGGGAACCATTTGAAGAATACCAAGAAAGCTCATATTTTTCTCAGTTTTA 972

Qy        177 GlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgVal 196
              |||||||||      |||   |||||||||:::         |||      :::||||||
Db        973 CAATGGAAATGGCTGGAAAGGCAACCCGTAACAAAGAACACATTTAGACATTACAGAGTT 1032

Qy        197 LeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMet 216
              |||||||||||||||||||||||||||||||||   ||||||:::   ||||||||||||
Db       1033 CTAGGAAAAGGCGGATTTGGAGAGGTTTGCGCCTGTCAAGTGCGAGCCACAGGAAAAATG 1092

Qy        217 TyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAla 236
              ||||||||||||||||||   |||||||||:::||||||:::   ||||||   ||||||
Db       1093 TATGCCTGCAAAAAGCTACAAAAAAAAAGAATAAAGAAGAGGAAAGGTGAAGCTATGGCT 1152

Qy        237 LeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyr 256
              |||   ||||||   |||||||||||||||   |||   |||:::|||||||||||||||
Db       1153 CTAAATGAGAAAAGAATTCTGGAGAAAGTGCAAAGTAGATTCGTAGTTAGTTTAGCCTAC 1212

Qy        257 AlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeu 276
              |||:::|||:::|||      ||||||||||||:::::::::||||||||||||||||||
Db       1213 GCTTATGAAACCAAAGATGCCTTGTGCTTGGTGCTCACCATTATGAATGGAGGGGATTTG 1272

Qy        277 LysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyr 296
              ||||||||||||||||||:::|||      |||   |||      |||   :::||||||
Db       1273 AAGTTTCACATTTACAACCTGGGCAATCCCGGCTTTGATGAGCAGAGAGCCGTTTTCTAT 1332

Qy        297 SerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAsp 316
              :::|||::::::   ||||||:::      |||            |||||||||||||||
Db       1333 GCTGCAGAGCTGTGTTGCGGCTTGGAAGATTTACAGAGGGAAAGAATTGTATACAGAGAC 1392

Qy        317 MetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGly 336
              :::||||||||||||:::||||||||||||   |||:::   |||:::||||||||||||
Db       1393 TTGAAGCCTGAGAATATTCTCCTTGATGATCGTGGACACATCCGGATTTCAGACCTCGGT 1452

Qy        337 LeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyr 356
              ||||||   |||:::      |||:::   :::      |||   ||||||   ||||||
Db       1453 TTGGCCACAGAGATCCCAGAAGGACAGAGGGTTCGAGGAAGAGTTGGAACAGTCGGCTAC 1512

Qy        357 MetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAla 376
              ||||||||||||::::::      :::      |||::::::      ||||||:::
Db       1513 ATGGCACCTGAAGTTGTCAATAATGAA---AAGTATACGTTTAGTCCCGATTGGTGGGGA 1569

Qy        377 MetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlu 396
              :::||||||   ||||||||||||:::   |||   :::|||||||||   |||||||||
Db       1570 CTTGGCTGTCTGATCTATGAAATGATTCAGGGACATTCTCCATTCAAAAAATACAAAGAG 1629

Qy        397 LysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHis 416
              ||||||      |||::::::   ||||||         |||      ::::::
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Qy        417 AspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGlu 436
              :::   |||:::|||:::||||||   |||||||||:::   |||   |||   |||
Db       1687 GAGAAGTTTTCAGAGGATGCCAAATCTATCTGCAGGATGTTACTCACCAAGAATCCAAGC 1746

Qy        437 GlnArgLeuGlySerArg---GluLysSerAspAspProArgLysHisHisPhePheLys 455
              :::|||||||||   |||   |||   :::         ::::::|||      ||||||
Db       1747 AAGCGGCTGGGCTGCAGGGGCGAGGGAGCGGCTGGGGTGAAGCAGCACCCCGTGTTCAAG 1806

Qy        456 ThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAspPro 475
                 |||||||||   ||||||||||||   ::::::||||||||||||   |||||||||
Db       1807 GACATCAACTTCAGGAGGCTGGAGGCAAACATGCTGGAGCCCCCTTTCTGTCCTGATCCT 1866

Qy        476 SerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGlyVal 495
                    ||||||   ||||||:::   :::|||:::   ||||||   |||:::|||:::
Db       1867 CATGCCGTTTACTGTAAGGACGTCCTGGATATCGAGCAGTTCTCGGCGGTGAAAGGATC 1926
```

```
Qy         496 GluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIle 515
                     |||      |||:::   |||:::      ||||||||||||   |||   |||
Db        1927 TACCTGGACACCGCAGATGAAGACTTCTATGCTCGGTTTGCTACCGGGTGTGTCTCCATC 1986

Qy         516 AlaTrpGln---Glu-GluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
                  ||||||   ||| ::::::||||||:::|||   |||:::::::::|||
Db        1987 CCCTGGCAGAATGAGGCAGATGATCGAATCTGGGTGTTTCAAAGACATCAAC 2038

RESULT 2
BC057206
LOCUS       BC057206                2989 bp    mRNA    linear   HTC 19-NOV-2003
DEFINITION  Mus musculus G protein-coupled receptor kinase 6, mRNA (cDNA clone
            IMAGE:5328461), containing frame-shift errors.
ACCESSION   BC057206
VERSION     BC057206.1  GI:34784381
KEYWORDS    HTC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2989)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 2989)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-AUG-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
            Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.
            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 123 Row: m Column: 10
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 7242151
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
     source          1..2989
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="NMRI"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5328461"
                     /tissue_type="Mammary tumor. WAP-Tag model. 5 months old,
                     gross tissue."
                     /clone_lib="NCI_CGAP_Mam4"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

Alignment Scores:
Pred. No.:               2.29e-112      Length:          2989
Score:                   1219.50        Matches:         240
Percent Similarity:      65.17%         Conservative:    108
Best Local Similarity:   44.94%         Mismatches:      161
Query Match:             42.21%         Indels:          25
DB:                      11             Gaps:            8

US-10-044-205A-2 (1-553) x BC057206 (1-2989)

Qy           7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSerAspCysAsp 26
               |||:::|||::::::|||||||||      |||:::||||||:::            :::
Db         174 CTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGTGGCGGGAAT 233

Qy          27 SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
                  |||         ::::::   |||:::   |||      |||   :::      |||
Db         234 CGCAAAGGCAAGAGCAAGAAATGGCGCCAGATGCTGCAGTTCCCCCATATCAGCCAGTGT 293

Qy          46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
                  |||||||||      |||      ::::::|||||||||||||||:::|||||||||
Db         294 GAGGAGCTTCGACTCAGCCTTGAGCGTGACTACCACAGCCTATGTGAGCGCCAGCCCATT 353

Qy          66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
               ||||||   |||||||||:::|||   ||||||   |||         :::
Db         354 GGGCGCCTGTTATTTCGTGAGTTCTGTGCTACGAGACCTGAGCTGACCCGGTGTACTGCC 413

Qy          86 PheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyProThrLysAspSerAla 105
               ||||||:::   |||      :::|||:::      :::         |||
Db         414 TTCCTGGATGGGGTGTCTGAATATGAGGTGACCCCTGATGAGAAGCGGAAAGCATGTGGG 473

Qy         106 ---------LeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGlyAsnPro 122
                        :::|||      ::::::                     |||      |||
Db         474 CGCCGACTAATGCAGAACTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGAAGTTCCA 533

Qy         123 GlnProPheLeuSerGlnAlaValAlaThr------------LysCysGlnAlaAlaThr 138
               :::      :::|||                              |||:::
Db         534 CGGCAGCTGGTGAGTAACTGTGCCCAGCGGCTAGAGCAGGGACCCTGCAAAGACCTCTTC 593

Qy         139 ThrGluGluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeu 158
                  |||      |||:::                                    :::|||
Db         594 CAGGAGCTGACCCGGCTG---------------------------ACCCACGAGTACCTG 626

Qy         159 GlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrp 178
                        ||||||   |||::::::   |||   ::::::::::::||||||||||||
Db         627 AGCACGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAACCGTTTTCTGCAGTGG 686

Qy         179 LysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGly 198
               |||      |||   |||||||||:::         |||   ::::::||||||||||||
Db         687 AAGTGGCTGGAAAGGCAACCAGTGACCAAAAACACCTTCAGGCAGTACCGAGTCCTGGGC 746

Qy         199 LysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAla 218
               |||||||||||||||||||||   |||               ||||||||||||||||||
Db         747 AAAGGTGGCTTTGGGGAGGTGCGGGCA---------------ACAGGCAAGATGTACGCA 791
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Qy        219 CysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeu 238
              ||||||||||||:::|||||||||:::||||||:::   ||||||   |||||||||
Db        792 TGCAAGAAACTGGAAAAGAAGCGGATAAAGAAGCGAAAGGGGGAGGCCATGGCTCTCAAC 851

Qy        239 GluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPhe 258
              ||||||:::|||||||||||||||:::|||   |||:::||||||||||||||||||:::
Db        852 GAGAAACAGATCTTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTTAGCCTACGCCTAT 911

Qy        259 GluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPhe 278
              |||:::|||      ||||||||||||::::::|||||||||||||||||||||||||||
Db        912 GAGACCAAGGATGCACTGTGCCTGGTGCTGACATTGATGAATGGAGGTGACCTAAAGTTC 971

Qy        279 HisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAla 298
              |||||||||::::::|||      |||         :::|||   :::||||||:::|||
Db        972 CACATCTACCACATGGGCCAGGCTGGCTTTCCTGAAGCACGTGCTGTCTTCTATGCTGCT 1031

Qy        299 GlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLys 318
              :::|||   ||||||:::      ||||||         |||||||||||||||:::|||
Db       1032 GAGATCTGCTGTGGCCTGGAAGACCTGCACCGGGAACGCATTGTGTACAGGGATCTAAAG 1091

Qy        319 ProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAla 338
              |||||||||:::||||||||||||   |||:::   |||:::||||||||||||||||||
Db       1092 CCAGAGAATATCCTTCTGGATGACCATGGCCACATTCGGATCTCGGACCTGGGACTGGCC 1151

Qy        339 ValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAla 358
              |||   :::      |||:::   |||      |||   ||||||   ||||||||||||
Db       1152 GTGCATGTGCCTGAGGGCCAGACCATCAAAGGCCGTGTGGGCACTGTGGGCTACATGGCT 1211

Qy        359 ProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGly 378
              ||||||::::::      :::      |||::::::      ||||||:::|||:::|||
Db       1212 CCAGAGGTGGTGAGGAATGAG---CGCTACACGTTCAGTCCTGACTGGTGGGCGCTAGGC 1268

Qy        379 CysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysVal 398
              |||   :::|||||||||:::||||||::::::||||||:::      |||:::|||:::
Db       1269 TGCCTCCTGTACGAGATGATCGCAGGTCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATA 1328

Qy        399 SerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsn 418
                 :::|||::::::   :::|||   :::::::::      :::         |||
Db       1329 AAGCGCGAAGAGGTG---GAGCGGCTGGTCAAGGAAGTGGCCGAGGAGTACACAGACCGC 1385

Qy        419 PheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArg 438
              |||:::   :::|||:::   :::|||         |||:::|||   |||   :::|||
Db       1386 TTTTCCTCACAGGCGCGCTCACTCTGTTCTCAGCTTCTTAGCAAGGACCCTGCTGAGCGC 1445

Qy        439 LeuGlySerArg---GluLysSerAspAspProArgLysHisHisPhePheLysThrIle 457
              ||||||   |||         :::   :::   ::::::|||      ||||||   :::
Db       1446 CTGGGGTGTCGTGGAGGTGGCGCCCGTGAGGTAAAGGAGCACCCCCTTTTCAAGAAACTG 1505

Qy        458 AsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerVal 477
              ||||||   ||||||   ||||||::::::||||||||||||   |||||||||
Db       1506 AATTTCAAGCGGCTGGGAGCTGGCATGCTAGAGCCACCTTTTAAGCCTGATCCCCAGGCT 1565

Qy        478 ValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPhe 497
              :::|||   ||||||:::   :::|||:::   ||||||   |||:::||||||:::
Db       1566 ATTTATTGCAAGGATGTCCTGGACATTGAACAGTTCTCTACAGTTAAAGGTGTGGATCTG 1625

Qy        498 AspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrp 517
              :::      |||:::   |||::::::   ||||||||||||:::|||   |||   |||
Db       1626 GAGCCCACAGACCAAGACTTCTACCAGAAGTTTGCCACAGGCAGTGTGTCCATCCCCTGG 1685

Qy        518 GlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
              |||   |||::::::||||||      |||:::|||||||||
Db       1686 CAGAATGAGATGGTGGAGACCGAGTGCTTCCAGGAACTCAAT 1727

RESULT 3
AK051405
LOCUS       AK051405                2978 bp    mRNA    linear   HTC 20-SEP-2003
DEFINITION  Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
            enriched library, clone:D130046K22 product:G PROTEIN-COUPLED
            RECEPTOR KINASE GRK6 (EC 2.7.1.-) homolog [Mus musculus], full
            insert sequence.
ACCESSION   AK051405
VERSION     AK051405.1  GI:26094516
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2978)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
```

```
FEATURES             Location/Qualifiers
     source          1..2978
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                     /db_xref="MGI:2419686"
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                     /clone="D130046K22"
                     /tissue_type="spinal ganglion"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="12 days embryo"
     misc_feature    256..1893
                     /note="G PROTEIN-COUPLED RECEPTOR KINASE GRK6 (EC 2.7.1.-)
                     homolog [Mus musculus] (SWISSPROT|O70293, evidence: FASTY,
                     100%ID, 96.9%length, match=1714)
                     putative"
ORIGIN

Alignment Scores:
Pred. No.:             2.88e-112       Length:          2978
Score:                 1218.50         Matches:         236
Percent Similarity:    67.20%          Conservative:    102
Best Local Similarity: 46.92%          Mismatches:      153
Query Match:           42.18%          Indels:          12
DB:                    11              Gaps:            6

US-10-044-205A-2 (1-553) x AK051405 (1-2978)

Qy          34 ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSer 53
               |||:::   |||      |||   :::      |||   |||||||||      |||
Db         250 CGCCAGATGCTGCAGTTCCCCCATATCAGCCAGTGTGAGGAGCTTCGACTCAGCCTTGAG 309

Qy          54 LeuAsnPheHisSerLeuCysGluGlnGlnProIleGlyArgArgLeuPheArgAspPhe 73
                  ::::::|||||||||||||||:::|||||||||||||||   |||||||||:::|||
Db         310 CGTGACTACCACAGCCTATGTGAGCGCCAGCCCATTGGGCGCCTGTTATTTCGTGAGTTC 369

Qy          74 LeuAlaThrValProThrPheArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrp 93
                  ||||||   |||         :::         ||||||:::   |||      :::
Db         370 TGTGCTACGAGACCTGAGCTGACCCGGTGTACTGCCTTCCTGGATGGGGTGTCTGAATAT 429

Qy          94 GluLeuAlaGluGluGlyProThrLysAspSerAla---------LeuGlnGlyLeuVal 110
               |||:::      :::         |||                  :::|||      :::
Db         430 GAGGTGACCCCTGATGAGAAGCGGAAAGCATGTGGGCGCCGACTAATGCAGAACTTTCTG 489

Qy         111 AlaThrCysAlaSerAlaProAlaProGlyAsnProGlnProPheLeuSerGlnAlaVal 130
               :::                     |||      |||:::      :::|||
Db         490 AGCCACACGGGTCCTGACCTCATCCCTGAAGTTCCACGGCAGCTGGTGAGTAACTGT--- 546

Qy         131 AlaThrLysCysGlnAlaAlaThrThrGluGluGluArgValAlaAla-ValThrLeuAr 150
               |||   :::   :::|||   |||   :::               |||       |||
Db         547 GCCCAGCGGCTAGAGGCAGGGACCCTGCAAAGACCTCTTCCAGGAGCTGACCCGGCTG-- 604

Qy         150 gLysAlaGluAlaMetAlaPheLeuGlnGluGlnProPheLysAspPheValThrSerAl 170
                                  :::|||         ||||||   |||::::::   |||
Db         605 ----------ACCCACGAGTACCTGAGCACGGCCCCTTTTGCCGACTACCTCGACAGCAT 654

Qy         170 aPheTyrAspLysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTy 190
                ::::::::::::|||||||||||||||      |||   |||||||||:::
Db         655 CTACTTCAACCGTTTTCTGCAGTGGAAGTGGCTGGAAAGGCAACCAGTGACCAAAAACAC 714

Qy         190 rPheThrGluPheArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnVa 210
                |||   ::::::|||||||||||||||||||||||||||||||||||||||   |||||
Db         715 CTTCAGGCAGTACCGAGTCCTGGGCAAAGGTGGCTTTGGGGAGGTATGTGCCTGCCAGGT 774

Qy         210 lLysAsnThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLy 230
               |:::   ||||||||||||||||||||||||||||||:::|||||||||:::||||||::
Db         775 GCGGGCAACAGGCAAGATGTACGCATGCAAGAAACTGGAAAAGAAGCGGATAAAGAAGCG 834

Qy         230 sGlyGlyGluLysMetAlaLeuLeuGluLysGluIleLeuGluLysValSerSerProPh 250
               :   ||||||   |||||||||   ||||||:::|||||||||||||||:::|||   ||
Db         835 AAAGGGGGAGGCCATGGCTCTCAACGAGAAACAGATCTTGGAGAAAGTGAACAGTAGGTT 894

Qy         250 eIleValSerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLe 270
               |:::||||||||||||||||||:::|||:::|||      ||||||||||||::::::||
Db         895 TGTAGTGAGCTTAGCCTACGCCTATGAGACCAAGGATGCACTGTGCCTGGTGCTGACATT 954

Qy         270 uMetAsnGlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMe 290
               ||||||||||||||||||||||||||||||||||::::::|||      |||
Db         955 GATGAATGGAGGTGACCTAAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTTCCTGA 1014

Qy         290 tSerArgValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLe 310
                :::|||   :::||||||:::|||:::|||   ||||||:::      ||||||
Db        1015 AGCACGTGCTGTCTTCTATGCTGCTGAGATCTGCTGTGGCCTGGAAGACCTGCACCGGGA 1074

Qy         310 uGlyIleValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCy 330
                   |||||||||||||||:::||||||||||||:::||||||||||||   |||:::
Db        1075 ACGCATTGTGTACAGGGATCTAAAGCCAGAGAATATCCTTCTGGATGACCATGGCCACAT 1134

Qy         330 sArgLeuSerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleThrGlnAr 350
                |||:::|||||||||||||||||||||   :::      |||:::   |||      ||
Db        1135 TCGGATCTCGGACCTGGGACTGGCCGTGCATGTGCCTGAGGGCCAGACCATCAAAGGCCG 1194

Qy         350 gAlaGlyThrAsnGlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTy 370
               |   ||||||   ||||||||||||||||||::::::      :::      |||:::::
Db        1195 TGTGGGCACTGTGGGCTACATGGCTCCAGAGGTGGTGAGGAATGAG---CGCTACACGTT 1251

Qy         370 rProValAspTrpPheAlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrPr 390
               :      ||||||:::|||:::||||||   :::|||||||||:::||||||::::::||
Db        1252 CAGTCCTGACTGGTGGGCGCTAGGCTGCCTCCTGTACGAGATGATCGCAGGTCAGTCGCC 1311

Qy         390 oPheLysAspTyrLysGluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAs 410
               ||||:::      |||:::|||:::   :::|||::::::   :::|||   ::::::::
Db        1312 CTTCCAGCAGAGGAAGAAGAAGATAAAGCGCGAAGAGGTG---GAGCGGCTGGTCAAGGA 1368

Qy         410 pGluValLysPheGlnHisAspAsnPheThrGluGluAlaLysAspIleCysArgLeuPh 430
               :      :::         |||   |||:::   :::|||:::   :::|||
Db        1369 AGTGGCCGAGGAGTACACAGACCGCTTTTCCTCACAGGCGCGCTCACTCTGTTCTCAGCT 1428

Qy         430 eLeuAlaLysLysProGluGlnArgLeuGlySerArg---GluLysSerAspAspProAr 449
                |||:::|||   |||   :::|||||||||   |||         :::   :::   ::
Db        1429 TCTTAGCAAGGACCCTGCTGAGCGCCTGGGGTGTCGTGGAGGTGGCGCCCGTGAGGTAAA 1488

Qy         449 gLysHisHisPhePheLysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluPr 469
               ::::|||      ||||||   :::||||||   ||||||   ||||||::::::|||||
Db        1489 GGAGCACCCCCTTTTCAAGAAACTGAATTTCAAGCGGCTGGGAGCTGGCATGCTAGAGCC 1548

Qy         469 oProPheValProAspProSerValValTyrAlaLysAspIleAlaGluIleAspAspPh 489
               |||||||   |||||||||      :::|||   ||||||:::   :::|||:::   ||
Db        1549 ACCTTTTAAGCCTGATCCCCAGGCTATTTATTGCAAGGATGTCCTGGACATTGAACAGTT 1608

Qy         489 eSerGluValArgGlyValGluPheAspAspLysAspLysGlnPhePheLysAsnPheAl 509
               ||||   |||:::||||||:::   :::      |||:::   |||::::::   |||||
Db        1609 CTCTACAGTTAAAGGTGTGGATCTGGAGCCCACAGACCAAGACTTCTACCAGAAGTTTGC 1668

Qy         509 aThrGlyAlaValProIleAlaTrpGlnGluGluIleIleGluThrGlyLeuPheGluGl 529
               |||||||:::|||   |||   ||||||   |||::::::||||||      |||:::||
Db        1669 CACAGGCAGTGTGTCCATCCCCTGGCAGAATGAGATGGTGGAGACCGAGTGCTTCCAGGA 1728

Qy         529 uLeuAsn 531
               |||||||
Db        1729 ACTCAAT 1735

RESULT 4
AY406080
LOCUS       AY406080                1721 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens GPRK5 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406080
VERSION     AY406080.1  GI:39762054
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1721)
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AUTHORS     Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE       Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
JOURNAL     Science 302 (5652), 1960-1963 (2003)
 PUBMED     14671302
REFERENCE   2  (bases 1 to 1721)
 AUTHORS    Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..1721
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1..>1721
                     /gene="GPRK5"
                     /locus_tag="HCM2438"
ORIGIN

Alignment Scores:
Pred. No.:                 7.1e-86        Length:         1721
Score:                     955.50         Matches:        198
Percent Similarity:        61.95%         Conservative:   82
Best Local Similarity:     43.81%         Mismatches:     141
Query Match:               33.07%         Indels:         31
DB:                        29             Gaps:           8

US-10-044-205A-2 (1-553) x AY406080 (1-1721)

Qy       37 LeuAlaLeuProGlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPhe 56
            |||      |||   :::      |||   :::||||||:::   :::      ::::::
Db       48 CTGAAGTTCCCTCACATTAGCCAGTGTGAAGACCTCCGAAGGACCATAGACAGAGATTAC 107

Qy       57 HisSerLeuCysGluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThr 76
               |||||||||::::::|||||||||||||||   |||||||||   |||      |||
Db      108 TGCAGTTTATGTGACAAGCAGCCAATCGGGAGGCTGCTTTTCCGGCAGTTTTGTGAAACC 167

Qy       77 ValProThrPheArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGlu------ 94
               |||                     ||||||:::   |||      :::|||
Db      168 AGGCCTGGGCTGGAGTGTTACATTCAGTTCCTGGACTCCGTGGCAGAATATGAAGTTACT 227

Qy       95 ------------LeuAlaGluGluGlyProThrLysAspSerAlaLeuGlnGlyLeuVal 110
                        |||   |||:::|||      |||:::         :::   |||
Db      228 CCAGATGAAAAACTGGGAGAGAAAGGG------AAGGAAATTATGACCAAGTACCTC--- 278

Qy      111 AlaThrCysAlaSerAlaProAlaProGlyAsnPro---------------------Gln 123
                                    |||   :::|||                     |||
Db      279 ---------------------ACCCCAAAGTCCCCTGTTTTCATAGCCCAAGTTGGCCAA 317

Qy      124 ProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGluGluGluArg 143
                  :::||||||                  |||            |||
Db      318 GACCTGGTCTCCCAGACGGAGGAGAAGCTCCTACAGAAGCCGTGCAAAGAACTCTTTTCT 377

Qy      144 ValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGluGlnProPhe 163
                  |||   ::::::   :::               :::|||:::   :::||||||
Db      378 GCCTGTGCACAGTCTGTCCACGAG---------------TACCTGAGGGGAGAACCATTC 422

Qy      164 LysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeuPheGluMet 183
               :::::::::   |||   |||:::|||:::|||||||||||||||      |||
Db      423 CACGAATATCTGGACAGCATGTTTTTGACCGCTTTCTCCAGTGGAAGTGGTTGGAAAGN 482

Qy      184 GlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGlyGlyPheGly 203
Db      483 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 542

Qy      204 GluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLysLysLeuAsp 223
               |||||||||   ||||||:::   ||||||||||||||||||||||||:::|||:::
Db      543 NNNGTCTGTGCCTGCCAGGTTCGGGCCACGGGTAAAATGTATGCCTGCAAGCGCTTGGAG 602

Qy      224 LysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLysGluIleLeu 243
            |||||||||:::||||||:::   ||||||   |||||||||   ||||||:::||||||
Db      603 AAGAAGAGGATCAAAAAGAGGAAAGGGGAGTCCATGGCCCTCAATGAGAAGCAGATCCTC 662

Qy      244 GluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSerLysThrHis 263
            |||||||||:::|||   |||:::|||:::||||||||||||:::|||:::|||
Db      663 GAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCCTATGCCTACGAGACCAAGGATGCA 722

Qy      264 LeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIleTyrAsnVal 283
            ||||||||||||:::::::::||||||||||||||||||||||||||||||||||||:::
Db      723 CTGTGCTTGGTCCTGACCATCATGAATGGGGGTGACCTGAAGTTCCACATCTACAACATG 782

Qy      284 GlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIleAlaCysGly 303
            |||      |||   :::      |||   :::||||||:::|||:::|||   ||||||
Db      783 GGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTTTATGCGGCAGAGATCCTCTGCGGC 842

Qy      304 MetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGluAsnValLeu 323
            :::      ||||||            ||||||||||||:::||||||||||||:::|||
Db      843 TTAGAAGACCTCCACCGTGAGAACACCGTCTACCGAGATCTGAAACCTGAAAACATCCTG 902

Qy      324 LeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGluMetLysGly 343
            |||||||||   |||:::   |||:::|||||||||||||||||||||::::::
Db      903 TTAGATGATTATGGCCACATTAGGATCTCAGACCTGGGCTTGGCTGTGAAGATCCCCGAG 962

Qy      344 GlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGluIleLeuMet 363
            |||      |||      |||   ||||||   ||||||||||||||||||:::|||
Db      963 GGAGACCTGATCCGCGGCCGGGTGGGCACTGTTGGCTACATGGCTCCAGAGGTCCTGAAC 1022

Qy      364 GluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSerIleTyrGlu 383
               :::      |||            |||::::::   :::||||||   |||||||||
Db     1023 AACCAG---AGGTACGGCCTGAGCCCCGACTACTGGGGCCTTGGCTGCCTCATCTATGAG 1079

Qy      384 MetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLysGluAspLeu 403
            |||:::   |||::::::||||||:::      ||||||||||||   :::|||::::::
Db     1080 ATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCAAGGAGAAGGTGAAGCGGGAGGAGGTG 1139

Qy      404 LysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThrGluGluAla 423
               :::|||   |||:::   |||      :::   |||      |||:::|||||||||
Db     1140 GACCGCCGGGTCCTGGAGACGGAGGAGGTGTACTCCCAC---AAGTTCTCCGAGGAGGCC 1196

Qy      424 LysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGlySerArgGlu 443
            |||   ||||||::::::   |||   |||      :::||||||||||||   :::|||
Db     1197 AAGTCCATCTGCAAGATGCTGCTCACGAAAGATGCGAAGCAGAGGCTGGGCTGCCAGGAG 1256

Qy      444 Lys---SerAspAspProArgLysHisHisPhePheLysThrIleAsnPheProArgLeu 462
            :::   :::   :::   ::::::|||   ||||||:::   :::||||||   ||||||
Db     1257 GAGGGGGCTGCAGAGGTCAAGAGACACCCCTTCTTCAGGAACATGAACTTCAAGCGCTTA 1316

Qy      463 GluAlaGlyLeuIleGluProProPheValProAsp 474
            |||||||||:::::::::||||||||||||||||||
Db     1317 GAAGCCGGGATGTTGGACCCTCCCTTCGTTCCAGAC 1352

RESULT 5
AY406082
LOCUS       AY406082                1721 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus GPRK5 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406082
VERSION     AY406082.1  GI:39762056
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1721)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1721)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..1721
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1..>1721
                     /gene="GPRK5"
                     /locus_tag="HCM2438"
ORIGIN

Alignment Scores:
Pred. No.:              2.37e-84      Length:         1721
Score:                  940.50        Matches:        193
Percent Similarity:     61.88%        Conservative:   83
Best Local Similarity:  43.27%        Mismatches:     151
Query Match:            32.55%        Indels:         19
DB:                     29            Gaps:           7

US-10-044-205A-2 (1-553) x AY406082 (1-1721)

Qy         37 LeuAlaLeuProGlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPhe 56
              |||      |||   :::      |||   :::||||||:::   :::      ::::::
Db         48 CTGAAGTTTCCTCACATCAGCCAGTGTGAAGACCTCCGAAGGACCATAGACAGAGATTAC 107

Qy         57 HisSerLeuCysGluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThr 76
              :::|||||||||::::::|||||||||||||||   |||||||||   |||      |||
Db        108 TACAGTCTATGTGACAAGCAACCAATTGGGAGACTGCTTTTTCGACAGTTCTGTGAAACC 167

Qy         77 ValProThrPheArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAla 96
                 |||                     ||||||:::   |||      :::|||:::
Db        168 AGGCCTGGGCTGGAGTGCTACATTCAGTTCCTGGACTTAGTGGCAGAATATGAAATTACT 227

Qy         97 GluGluGlyProThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAla 116
                       |||   ::::::         :::|||
Db        228 ---------CCAGATGAAAACCTTGGGGCGAAGGGG---AAGGAAATAATGACCAAGTAC 275

Qy        117 ProAlaProGlyAsnPro---------------------GlnProPheLeuSerGlnAla 129
                    |||   :::|||                     |||      :::||||||
Db        276 CTCACTCCAAAGTCCCCAGTCTTCATTGCCCAAGTTGGACAGGACCTGGTCTCCCAGACA 335

Qy        130 ValAlaThrLysCysGlnAlaAlaThrThrGluGluGluArgValAlaAlaValThrLeu 149
                             |||:::         |||               |||   ::::::
Db        336 GAGAAGAAGCTCCTGCAGAGCCCCTGCAAAGAACTCTTCTCTGCTTGTGCTCAGTCTGTC 395

Qy        150 ArgLysAlaGluAlaMetAlaPheLeuGlnGluGlnProPheLysAspPheValThrSer 169
                                   :::|||:::      ||||||   :::::::::   |||
Db        396 CATGAC---------------TACTTGAAGGGAGACCCCTTCCACGAGTACCTGGATAGC 440

Qy        170 AlaPheTyrAspLysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLys 189
                 ::::::|||:::|||||||||||||||      |||
Db        441 ATGTATTTTGACCGTTTTCTGCAGTGGAAATGGTTAGAAAGNNNNNNNNNNNNNNNNNNN 500

Qy        190 TyrPheThrGluPheArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGln 209
                                                           |||||||||   |||
Db        501 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTCTGTGCCTGCCAG 560

Qy        210 ValLysAsnThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLys 229
              |||:::   ||||||||||||||||||||||||:::|||:::|||||||||:::||||||
Db        561 GTTCGGGCCACTGGTAAAATGTATGCTTGTAAACGCTTAGAGAAGAAGAGGATCAAAAAG 620

Qy        230 LysGlyGlyGluLysMetAlaLeuLeuGluLysGluIleLeuGluLysValSerSerPro 249
              :::   ||||||   |||||||||   ||||||:::|||||||||||||||:::|||
Db        621 AGGAAAGGCGAATCCATGGCACTCAACGAAAAGCAGATTCTTGAGAAGGTCAACAGCCAG 680

Qy        250 PheIleValSerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSer 269
              |||:::|||:::||||||||||||:::|||:::|||      ||||||||||||::::::
Db        681 TTTGTGGTCAACCTGGCCTATGCCTATGAAACCAAAGATGCACTATGCCTGGTTCTGACC 740

Qy        270 LeuMetAsnGlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAsp 289
              :::||||||||||||||||||||||||||||||||||||:::|||      |||   :::
Db        741 ATTATGAATGGTGGTGACCTGAAGTTTCACATCTACAATATGGGGAATCCTGGCTTTGAG 800

Qy        290 MetSerArgValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGlu 309
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Db        801 GAAGAGCGAGCCTTATTTATGCAGCTGAGATCCTCTGTGGCCTAGAAGACTTACACCGT 860

Qy        310 LeuGlyIleValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsn 329
                       ||||||||||||:::||||||||||||:::||||||||||||   |||:::
Db        861 GAGAACACTGTCTATAGAGATCTAAAACCCGAAAACATCTTGCTGGATGATTATGGCCAC 920

Qy        330 CysArgLeuSerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleThrGln 349
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Db        921 ATAAGGATCTCAGACCTCGGACTGGCCGTGAAGATCCCCGAGGGAGACCTTATCCGTGGC 980

Qy        350 ArgAlaGlyThrAsnGlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSer 369
              |||   ||||||   ||||||||||||||||||:::|||      :::      |||
Db        981 CGGGTAGGCACTGTTGGCTACATGGCCCCAGAAGTTCTGAACAACCAG---CGATATGGA 1037

Qy        370 TyrProValAspTrpPheAlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThr 389
                       |||::::::   :::||||||   ||||||||||||:::   |||::::::
Db       1038 CTGAGCCCTGACTACTGGGGCCTGGGCTGCCTCATCTATGAGATGATTGAAGGCCAGTCA 1097

Qy        390 ProPheLysAspTyrLysGluLysValSerLysGluAspLeuLysGlnArgThrLeuGln 409
              ||||||:::      ||||||||||||   :::|||::::::   :::|||   |||:::
Db       1098 CCATTTCGAGGTCGCAAGGAGAAGGTTAAGCGGGAAGAGGTGGATCGCCGGGTGCTGGAG 1157

Qy        410 AspGluValLysPheGlnHisAspAsnPheThrGluGluAlaLysAspIleCysArgLeu 429
                 |||      :::            |||:::||||||||||||   ||||||   :::
Db       1158 ACTGAGGAAGTATATTCC---TCCAAGTTCTCTGAAGAGGCCAAGTCCATCTGCAACATG 1214

Qy        430 PheLeuAlaLysLysProGluGlnArgLeuGlySerArgGluLys---SerAspAspPro 448
                 |||   |||      :::||||||||||||   :::|||:::   :::   :::
Db       1215 CTGCTCACCAAAGACTCGAAGCAGAGGCTGGGCTGCCAGGAGGAGGGGGCCGCCGAGGTC 1274

Qy        449 ArgLysHisHisPhePheLysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGlu 468
              ::::::|||   ||||||:::   :::||||||   |||||||||||||||:::::::::
Db       1275 AAGAGGCACCCTTTCTTCAGGAACATGAACTTTAAGCGCCTGGAGGCTGGGATGTTGGAC 1334

Qy        469 ProProPheValProAsp 474
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Db       1335 CCTCCCTTCGTTCCAGAT 1352

RESULT 6
BX404586/c
LOCUS       BX404586                1201 bp    mRNA    linear   EST 13-MAY-2003
DEFINITION  BX404586 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
            CS0DA004YM05 3-PRIME, mRNA sequence.
ACCESSION   BX404586
VERSION     BX404586.1  GI:30648023
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
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                    Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
                    Library was constructed by Life Technologies, a division of
                    Invitrogen. This sequence belongs to sequence cluster 3090.f For
                    more information about this cluster, see
                    http://www.genoscope.cns.fr/
                    cgi-bin/cluster.cgi?seq=CS0AA004AG03NP1&cluster=3090.f. Contact :
                    Feng Liang Email : fliang@lifetech.com URL :
                    http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                    Faraday Avenue Genoscope sequence ID : CS0AA004AG03NP1.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DA004YM05"
                     /tissue_type="NEUROBLASTOMA"
                     /clone_lib="Homo sapiens NEUROBLASTOMA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

Alignment Scores:
Pred. No.:              8.96e-79        Length:         1201
Score:                  883.50          Matches:        166
Percent Similarity:     74.59%          Conservative:   63
Best Local Similarity:  54.07%          Mismatches:     75
Query Match:            30.58%          Indels:         3
DB:                     13              Gaps:           3

US-10-044-205A-2 (1-553) x BX404586 (1-1201)

Qy        175 PheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPhe 194
              |||||||||||||||      |||   |||||||||:::         |||   ::::::
Db       1003 TTCCTGCAGTGGAAGTGGCTGGAAARGCAGCCAGTGACCAAAAACACCTTCAAGCAATAC 944

Qy        195 ArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGly 214
              |||||||||||||||||||||||||||||||||||||||   ||||||:::   ||||||
Db        943 CGAGTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGGT 884

Qy        215 LysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLys 234
              ||||||||||||||||||||||||:::|||||||||:::||||||:::   ||||||
Db        883 AAGATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAGGCC 824

Qy        235 MetAlaLeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeu 254
              |||||||||   ||||||:::|||||||||||||||:::|||   |||:::|||||||||
Db        823 ATGGCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTTG 764

Qy        255 AlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGly 274
              |||||||||:::|||:::|||      ||||||||||||::::::|||||||||||||||
Db        763 GCCTACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGGC 704

Qy        275 AspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIle 294
              |||||||||||||||||||||::::::|||      |||         :::|||   :::
Db        703 GACCTCAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGCCGTC 644

Qy        295 PheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyr 314
              ||||||:::|||:::|||   ||||||:::      ||||||         |||||||||
Db        643 TTCTACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTAC 584

Qy        315 ArgAspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAsp 334
              ||||||:::||||||||||||:::||||||||||||   |||:::   |||:::||||||
Db        583 AGGGACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTCTGAC 524

Qy        335 LeuGlyLeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsn 354
              |||||||||||||||   :::      |||:::   |||      |||   ||||||
Db        523 CTGGGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTG 464

Qy        355 GlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrp 374
              ||||||||||||||||||::::::   :::      |||::::::      ||||||
Db        463 GGTTACATGGCTCCGGAGGTGGTGAAGAATGAA---CGGTACACGTTCAGCCCTGACTGG 407

Qy        375 PheAlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyr 394
              :::|||:::||||||   :::|||||||||:::||||||::::::||||||:::
Db        406 TGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCAGAGG 347

Qy        395 LysGluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPhe 414
              |||:::|||:::   :::|||::::::   :::|||   :::::::::      :::
Db        346 AAGAAGAAGATCAAGCGGGAGGAGGTG---GAGCGGCTGGTGAAGGAGGTCCCCGAGGAG 290

Qy        415 GlnHisAspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLys 434
                    :::   |||:::   :::|||:::   :::|||         |||   |||
Db        289 TATTCCGAGCGCTTTTCCCCGCAGGCCCGCTCACTTTGCTCACAGCTCCTCTGCAAGGAC 230

Qy        435 ProGluGlnArgLeuGlySerArgGluLysSer---AspAspProArgLysHisHisPhe 453
              |||   :::|||||||||   |||      |||      :::   ::::::|||
Db        229 CCTGCCGAACGCCTGGGGTGTCGTGGGGGCAGTGCCCGCGAGGTGAAGGAGCACCCCCTC 170

Qy        454 PheLysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValPro 473
              ||||||   :::||||||   ||||||   ||||||::::::||||||||||||   |||
Db        169 TTTAAGAAGCTGAACTTCAAGCGGCTGGGAGCTGGCATGCTGGAGCCGCCCTTCAAGCCT 110

Qy        474 AspProSerValValTyrAla 480
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Db        109 GACGTGAGTGCAGCCCACTCC 89

RESULT 7
BQ066445
LOCUS       BQ066445                 968 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6861074 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5931090
            5', mRNA sequence.
ACCESSION   BQ066445
VERSION     BQ066445.1  GI:19895491
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 968)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2111  row: n  column: 19
            High quality sequence stop: 636.
FEATURES             Location/Qualifiers
     source          1..968
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5931090"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_99"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

Alignment Scores:
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Pred. No.:              4.12e-73    Length:         968
Score:                  826.50      Matches:        158
Percent Similarity:     70.97%      Conservative:   62
Best Local Similarity:  50.97%      Mismatches:     79
Query Match:            28.61%      Indels:         11
DB:                     13          Gaps:           5

US-10-044-205A-2 (1-553) x BQ066445 (1-968)

Qy        236 AlaLeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAla 255
              ||||||   ||||||:::|||||||||||||||:::|||   |||:::|||:::||||||
Db          3 GCCCTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCC 62

Qy        256 TyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAsp 275
              ||||||:::|||:::|||      ||||||||||||:::::::::|||||||||||||||
Db         63 TATGCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGAC 122

Qy        276 LeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePhe 295
              |||||||||||||||||||||:::|||      |||   :::      |||   :::|||
Db        123 CTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTT 182

Qy        296 TyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArg 315
              |||:::|||:::|||   ||||||:::      ||||||            |||||||||
Db        183 TATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGA 242

Qy        316 AspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeu 335
              |||:::||||||||||||:::||||||||||||   |||:::   |||:::|||||||||
Db        243 GATCTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTG 302

Qy        336 GlyLeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGly 355
              ||||||||||||::::::      |||      |||      |||   ||||||   |||
Db        303 GGCTTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGCACTGTTGGC 362

Qy        356 TyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPhe 375
              |||||||||||||||:::|||      :::      |||               |||::::::
Db        363 TACATGGCTCCAGAGGTCCTGAACAACCAG---AGGTACGGCCTGAGCCCCGACTACTGG 419

Qy        376 AlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLys 395
                 :::||||||   ||||||||||||:::   |||::::::||||||:::      |||
Db        420 GGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCAAG 479

Qy        396 GluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGln 415
              |||||||||   :::|||::::::   :::|||   |||:::   |||      :::
Db        480 GAGAAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGGAGGAGGTGTACTCC 539

Qy        416 HisAspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysPro 435
              |||      |||:::||||||||||||   ||||||::::::   |||   |||
Db        540 CAC---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACGAAAGATGCG 596

Qy        436 GluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHisHisPhePhe 454
              :::||||||||||||   :::|||:::   :::   :::   ::::::|||   ||||||
Db        597 AAGCAGAGGCTGGGCTGCCAGGAGGAGGGGGCTGCAGAGGTCAAGAGACACCCCTTCTTC 656

Qy        455 LysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAsp 474
              :::   :::||||||   |||||||||||||||:::::::::||||||||||||||||||
Db        657 AGGAACATGAACTTCAAGCGCTTAGAAGCCGGGATGTTGGACCCTCCCTTCGTTCCAGAC 716

Qy        475 ProSerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGly 494
              |||      ||||||   ||||||:::   :::|||:::   ||||||   |||:::|||
Db        717 CCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACTGTGAAGGGC 776

Qy        495 ValGluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValPro 514
              |||      |||      |||      |||:::         |||:::||||||:::|||
Db        777 GTCAATCTGGACCACACAGACGACTTCTACTCCAAGTTCTCCACGGGCTCTGTGGTC 836

Qy        515 IleAlaTrpGlnGluGluIleIleGluThrGlyLeuPheGlu------------------ 528
              |||   ||||||   ::::::|||||||||         |||:::
Db        837 ATCCCATGGCAAAACCAGATGATAGAAACCGAATGCTTTAAAGGACCTGAACCTGGTTTG 896

Qy        529 GluLeuAsnAspProAsnArgProThrGly 538
              |||||||||            |||:::|||
Db        897 GAACTTAAT------GGTACCCCTTCCGGC 920
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RESULT 8
BQ057613
LOCUS       BQ057613                 998 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_7047352 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813275
            5', mRNA sequence.
ACCESSION   BQ057613
VERSION     BQ057613.1  GI:19816953
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 998)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2065  row: a  column: 20
            High quality sequence stop: 753.
FEATURES             Location/Qualifiers
     source          1..998
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5813275"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_99"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.09e-72    Length:         998
Score:                  822.50      Matches:        159
Percent Similarity:     70.87%      Conservative:   60
Best Local Similarity:  51.46%      Mismatches:     80
Query Match:            28.47%      Indels:         10
DB:                     13          Gaps:           4

US-10-044-205A-2 (1-553) x BQ057613 (1-998)

Qy        236 AlaLeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAla 255
              ||||||   ||||||:::|||||||||||||||:::|||   |||:::|||:::||||||
Db          3 GCCCTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCC 62

Qy        256 TyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAsp 275
              ||||||:::|||:::|||      ||||||||||||:::::::::|||||||||||||||
Db         63 TATGCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGAC 122

Qy        276 LeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePhe 295
              |||||||||||||||||||||:::|||      |||   :::      |||   :::|||
Db        123 CTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTT 182

Qy        296 TyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArg 315
              |||:::|||:::|||   ||||||:::      ||||||            |||||||||
Db        183 TATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGA 242
```

```
Qy          316 AspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeu 335
                |||:::||||||||||||:::||||||||||||   |||:::   |||:::|||||||||
Db          243 GATCTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTG 302

Qy          336 GlyLeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGly 355
                ||||||||||||::::::      |||      |||      |||   ||||||   |||
Db          303 GGCTTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGCACTGTTGGC 362

Qy          356 TyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPhe 375
                |||||||||||||||:::|||      :::      |||            |||::::::
Db          363 TACATGGCTCCAGAGGTCCTGAACAACCAG---AGGTACGGCCTGAGCCCCGACTACTGG 419

Qy          376 AlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLys 395
                   :::||||||   ||||||||||||:::   |||::::::||||||:::      |||
Db          420 GGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCAAG 479

Qy          396 GluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGln 415
                |||||||||   :::|||::::::   :::|||   |||:::   |||      :::
Db          480 GAGAAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGGAGGAGGTGTACTCC 539

Qy          416 HisAspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysPro 435
                |||      |||:::||||||||||||   ||||||::::::   |||   |||
Db          540 CAC---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACGAAAGATGCG 596

Qy          436 GluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHisHisPhePhe 454
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Db          597 AAGCAGAGGCTGGGCTGCCAGGAGGAGGGGGCTGCAGAGGTCAAGAGACACCCCTTCTTC 656

Qy          455 LysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAsp 474
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Db          657 AGGAACATGAACTTCAAGCGCTTAGAAGCCGGGATGTTGGACCCTCCCTTCGTTCCAGAC 716

Qy          475 ProSerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGly 494
                |||      ||||||   ||||||:::   :::|||:::   ||||||   |||:::|||
Db          717 CCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACTGTGAAGGGC 776

Qy          495 ValGluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValPro 514
                |||      |||      |||   :::            |||:::||||||:::|||
Db          777 GTCAATCTGGACCACACAGACGACGAACTTCTACTCAAGTTCTCCACGGGCTCTGTGTCC 836

Qy          515 IleAlaTrpGlnGluGluIleIleGluThr-GlyLeuPheGluGluLeuAsn-------- 531
                |||   ||||||   |||:::|||||||||       |||:::|||||||||
Db          837 ATCCCATGGCAAAACGAGATGATAGAAACAGAATGCTTTAAAGAGCTGAACGTGTTTGG 896

Qy          532 ----------AspProAsnArgPro 536
                             |||   ||||||
Db          897 AACCTAATGGTACCCTCCCCGCCCA 921

RESULT 9
BQ061150
LOCUS       BQ061150                1017 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6862973 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920182
            5', mRNA sequence.
ACCESSION   BQ061150
VERSION     BQ061150.1  GI:19884936
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1017)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2083  row: h  column: 07
            High quality sequence stop: 697.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5920182"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_99"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

Alignment Scores:
Pred. No.:              9.22e-72        Length:         1017
Score:                  813.50          Matches:        154
Percent Similarity:     71.72%          Conservative:   59
Best Local Similarity:  51.85%          Mismatches:     81
Query Match:            28.16%          Indels:         3
DB:                     13              Gaps:           3

US-10-044-205A-2 (1-553) x BQ061150 (1-1017)

Qy          236 AlaLeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAla 255
                ||||||   ||||||:::|||||||||||||||:::|||   |||:::|||:::||||||
Db            3 GCCCTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCC 62

Qy          256 TyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAsp 275
                ||||||:::|||:::|||      ||||||||||||:::::::::|||||||||||||||
Db           63 TATGCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGAC 122

Qy          276 LeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePhe 295
                |||||||||||||||||||||:::|||      |||   :::      |||   :::|||
Db          123 CTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTT 182

Qy          296 TyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArg 315
                |||:::|||:::|||   ||||||:::      ||||||            |||||||||
Db          183 TATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGA 242

Qy          316 AspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeu 335
                |||:::||||||||||||:::||||||||||||   |||:::   |||:::|||||||||
Db          243 GATCTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTG 302

Qy          336 GlyLeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGly 355
                ||||||||||||::::::      |||      |||      |||   ||||||   |||
Db          303 GGCTTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGCACTGTTGGC 362

Qy          356 TyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPhe 375
                |||||||||||||||:::|||      :::      |||            |||::::::
Db          363 TACATGGCTCCAGAGGTCCTGAACAACCAG---AGGTACGGCCTGAGCCCCGACTACTGG 419

Qy          376 AlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLys 395
                   :::||||||   ||||||||||||:::   |||::::::||||||:::      |||
Db          420 GGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCAAG 479

Qy          396 GluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGln 415
                |||||||||   :::|||::::::   :::|||   |||:::   |||      :::
Db          480 GAGAAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGGAGGAGGTGTACTCC 539

Qy          416 HisAspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysPro 435
                |||      |||:::||||||||||||   ||||||::::::   |||   |||
Db          540 CAC---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACGAAAGATGCG 596

Qy          436 GluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHisHisPhePhe 454
```

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                :::||||||||||||   :::|||:::   :::   :::   ::::::|||   ||||||
Db          597 AAGCAGAGGCTGGGCTGCCAGGAGGAGGGGCTGCAGAGGTCAAGAGACACCCCTTCTTC 656

Qy          455 LysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAsp 474
                :::   :::||||||   |||||||||||||||:::::::::||||||||||||||||||
Db          657 AGGAACATGAACTTCAAGCGCTTAGAAGCCGGGATGTTGGACCCTCCCTTCGTTCCAGAC 716

Qy          475 ProSerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGly 494
                |||      ||||||   ||||||:::   :::|||:::   ||||||         |||
Db          717 CCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACTGGTGAAGGC 776

Qy          495 ValGluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValPro 514
                |||      |||      |||      |||:::      |||:::||||||:::|||
Db          777 GTCAATCTGGACCACACAGACGACGACTTCTACTCCAAGTTCTCCACGGGCTCTGTGTCC 836

Qy          515 IleAlaTrpGlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
                |||            |||:::|||||||||      |||:::|||||||||
Db          837 ATCCCATGNGCAAACGAGATGATAGAAACAGAATGCTTTAAGGAGCTGAAC 887

RESULT 10
BQ061148
LOCUS       BQ061148                1019 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6862941 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920180
            5', mRNA sequence.
ACCESSION   BQ061148
VERSION     BQ061148.1  GI:19884933
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2083  row: h  column: 05
            High quality sequence stop: 704.
FEATURES             Location/Qualifiers
     source          1..1019
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5920180"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_99"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

Alignment Scores:
Pred. No.:              9.58e-71      Length:          1019
Score:                  803.50        Matches:         151
Percent Similarity:     72.54%        Conservative:    55
Best Local Similarity:  53.17%        Mismatches:      77
Query Match:            27.81%        Indels:          1
DB:                     13            Gaps:            1

US-10-044-205A-2 (1-553) x BQ061148 (1-1019)

Qy          157 PheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeu 176
                :::|||         ||||||   |||::::::   |||   ::::::::::::||||||
Db           15 TACCTGAGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAACCGTTTCCTG 74

Qy          177 GlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgVal 196
                |||||||||      |||   |||||||||:::         |||   ::::::||||||
Db           75 CAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTC 134

Qy          197 LeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMet 216
                |||||||||||||||||||||||||||||||||   ||||||:::   ||||||||||||
Db          135 CTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATG 194

Qy          217 TyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAla 236
                ||||||||||||||||||:::|||||||||:::||||||:::   ||||||   ||||||
Db          195 TATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCG 254

Qy          237 LeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyr 256
                |||   ||||||:::|||||||||||||||:::|||   |||:::|||||||||||||||
Db          255 CTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTAC 314

Qy          257 AlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeu 276
                |||:::|||:::|||      ||||||||||||::::::|||||||||||||||||||||
Db          315 GCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTC 374

Qy          277 LysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyr 296
                |||||||||||||||::::::|||      |||         :::|||   :::||||||
Db          375 AAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTAC 434

Qy          297 SerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAsp 316
                :::|||:::|||   ||||||:::      ||||||         |||||||||||||||
Db          435 GCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGAC 494

Qy          317 MetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGly 336
                :::||||||||||||:::||||||||||||   |||:::   |||:::|||||||||
Db          495 CTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTCTGACCTGNGA 554

Qy          337 LeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyr 356
                |||||||||   :::      |||:::   |||      |||   ||||||   ||||||
Db          555 CTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTAC 614

Qy          357 MetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAla 376
                ||||||||||||::::::      :::      |||::::::      ||||||:::|||
Db          615 ATGGCTCCGGAGGTGGTGAAGAATGAA---CGGTACACGTTCAGCCCTGACTGGTGGGCG 671

Qy          377 MetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlu 396
                :::||||||   :::|||||||||:::||||||::::::||||||:::      |||:::
Db          672 CTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAG 731

Qy          397 LysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHis 416
                |||:::   :::                        :::         |||
Db          732 AAAATCAAGCGGGGAGGAGGTGGAGCGGCTGGGTGAAGGAAGTCCCCGAAGAGTATTCCG 791

Qy          417 AspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGlu 436
                      |||:::   :::|||:::   :::|||         |||   |||   |||
Db          792 AGCGCTTTTTCCCCGCAGGCCCGCTCACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCC 851

Qy          437 GlnArgLeuGly 440
                :::|||||||||
Db          852 GAACGCCTGGGG 863

RESULT 11
BQ063841
LOCUS       BQ063841                1028 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6832078 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5925495
            5', mRNA sequence.
ACCESSION   BQ063841
VERSION     BQ063841.1  GI:19891943
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1028)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2097  row: e  column: 16
            High quality sequence stop: 604.
FEATURES             Location/Qualifiers
     source          1. .1028
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5925495"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_99"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

Alignment Scores:
Pred. No.:              4.99e-70        Length:         1028
Score:                  796.50          Matches:        155
Percent Similarity:     69.58%          Conservative:   60
Best Local Similarity:  50.16%          Mismatches:     84
Query Match:            27.57%          Indels:         10
DB:                     13              Gaps:           4

US-10-044-205A-2 (1-553) x BQ063841 (1-1028)

Qy         236 AlaLeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAla 255
               ||||||   ||||||:::|||||||||||||||:::|||   |||:::|||:::||||||
Db           3 GCCCTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCC 62

Qy         256 TyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAsp 275
               ||||||:::|||:::|||      ||||||||||||:::::::::|||||||||||||||
Db          63 TATGCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGAC 122

Qy         276 LeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePhe 295
               |||||||||||||||||||||:::|||      |||   :::      |||   :::|||
Db         123 CTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTT 182

Qy         296 TyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArg 315
               |||:::|||:::|||   ||||||:::      ||||||            |||||||||
Db         183 TATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGA 242

Qy         316 AspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeu 335
               |||:::||||||||||||:::||||||||||||   |||:::   |||:::|||||||||
Db         243 GATCTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTG 302

Qy         336 GlyLeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGly 355
               ||||||||||||::::::      |||      |||      |||   ||||||   |||
Db         303 GGCTTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGCACTGTTGGC 362

Qy         356 TyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPhe 375
               |||||||||||||||:::|||      :::      |||            |||::::::
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Db         363 TACATGGCTCCAGAGGTCCTGAACAACCAG---AGGTACGGCCTGAGCCCCGACTACTGG 419

Qy         376 AlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLys 395
                  :::||||||   ||||||||||||:::   |||::::::||||||:::      |||
Db         420 GGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCAAG 479

Qy         396 GluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGln 415
               |||||||||   :::|||::::::   :::|||   |||:::   |||      :::
Db         480 GAGAAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGGAGGAGGTGTACTCC 539

Qy         416 HisAspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysPro 435
               |||      |||:::||||||||||||   ||||||::::::   |||
Db         540 CAC---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACGANAGATGCG 596

Qy         436 GluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHisHisPhePhe 454
               :::||||||||||||   :::|||:::   :::   :::   ::::::|||   ||||||
Db         597 AAGCAGAGGCTGGGCTGCCAGGAGGAGGGGGCTGCAGAGGTCAAGAGACACCCCTTCTTC 656

Qy         455 LysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAsp 474
               :::   :::||||||   |||||||||||||||:::::::::||||||||||||||||||
Db         657 AGGAACATGAACTTCAAGCGCTTAGAAGCCGGGATGTTGGACCCTCCCTTCGTTCCAGAC 716

Qy         475 ProSerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGly 494
               |||      ||||||   ||||||:::   :::|||:::   ||||||
Db         717 CCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACTGGTGAGGNN 776

Qy         495 ValGluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValPro 514
                                 |||      |||:::      |||:::||||||:::|||
Db         777 CGTCATCTGGNACACACAGACGACGACTTCTACTCCAAGTTCTCCACGGGCTCTGTGTCC 836

Qy         515 IleAlaTrpGlnGluGluIleIleGluThrGlyLeuPheGlu-GluLeuAsn-------- 531
               |||   ||||||   |||:::||||||||||||      |||::: |||||||||
Db         837 ATCCCATGGCAAAACGAGATGATAGAAACAGAATGCTTTAAGGGAGCTGAACGTGTTTGG 896

Qy         532 ----------AspProAsnArgPro 536
                            |||:::||||||
Db         897 AACCTAATGGTACCCCTCCCGNCCA 921

RESULT 12
BU526699
LOCUS       BU526699                 934 bp    mRNA    linear   EST 13-SEP-2002
DEFINITION  AGENCOURT_10181837 NIH_MGC_101 Homo sapiens cDNA clone
            IMAGE:6536408 5', mRNA sequence.
ACCESSION   BU526699
VERSION     BU526699.1  GI:22837140
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 934)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2697  row: l  column: 08
            High quality sequence stop: 640.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6536408"
                     /tissue_type="epidermoid carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_101"
                     /note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
                     XhoI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

Alignment Scores:
Pred. No.:              9.92e-70        Length:         934
Score:                  793.00          Matches:        151
Percent Similarity:     71.93%          Conservative:   54
Best Local Similarity:  52.98%          Mismatches:     78
Query Match:            27.45%          Indels:         2
DB:                     13              Gaps:           2

US-10-044-205A-2 (1-553) x BU526699 (1-934)

Qy        157 PheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeu 176
              :::|||:::   :::||||||   :::::::::   |||   |||:::|||:::||||||
Db         78 TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTGACCGCTTTCTC 137

Qy        177 GlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgVal 196
              |||||||||      |||   |||||||||:::         |||   ::::::||||||
Db        138 CAGTGGAAGTGGTTGGAAAGGCAACCGGTGACCAAAAACACTTTCAGGCAGTATCGAGTG 197

Qy        197 LeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMet 216
              |||||||||||||||||||||||||||||||||   ||||||:::   ||||||||||||
Db        198 CTAGGAAAAGGGGGCTTCGGGGAGGTCTGTGCCTGCCAGGTTCGGGCCACGGGTAAAATG 257

Qy        217 TyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAla 236
              ||||||||||||:::|||:::|||||||||:::||||||:::   ||||||   ||||||
Db        258 TATGCCTGCAAGCGCTTGGAGAAGAAGAGGATCAAAAAGAGGAAAGGGGAGTCCATGGCC 317

Qy        237 LeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyr 256
              |||   ||||||:::|||||||||||||||:::|||   |||:::|||:::|||||||||
Db        318 CTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCCTAT 377

Qy        257 AlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeu 276
              |||:::|||:::|||      ||||||||||||:::::::::||||||||||||||||||
Db        378 GCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGACCTG 437

Qy        277 LysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyr 296
              ||||||||||||||||||:::|||      |||   :::      |||   :::||||||
Db        438 AAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTTTAT 497

Qy        297 SerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAsp 316
              :::|||:::|||   ||||||:::      ||||||            ||||||||||||
Db        498 GCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGAGAT 557

Qy        317 MetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGly 336
              :::||||||||||||:::||||||||||||   |||:::      |||:::|||||||||
Db        558 CTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTGGGC 617

Qy        337 LeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyr 356
              |||||||||::::::      |||      |||      |||   ||||||   ||||||
Db        618 TTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGNCGGGTGGGCACTGTTGGCTAC 677

Qy        357 MetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAla 376
              ||||||||||||:::|||      :::      |||            |||::::::
Db        678 ATGGCTCCAGAGGTCCTGAAACACCAG---AGGTACGGCCTGAGCCCCGACTACTGGGGC 734

Qy        377 MetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlu 396
              :::||||||   ||||||||||||:::   |||::::::||||||:::      ||||||
Db        735 CTTGGCTGCCTCATCTATGAGATGATCGAAGGCCAGTCGCCGTTCCGCGGNCGCAAGGAG 794

Qy        397 LysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHis 416
              ||||||   :::                                    :::
Db        795 AAAGTGAAGCGGGNAGGAAGTGGACCCGCCGGTTCCTGGAGACGGGAGGAGTGTACTCCC 854

Qy        417 AspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLys---Pro 435
                 :::|||:::|||      :::   ||||||::::::   |||   ||||||
Db        855 ACAAGTTTCTCCGAAGGAGGCCAGTCCATCTGCAAGATGCTGCTCACGAAAAAATGCCNA 914

Qy        436 GluGlnArgLeuGly 440
                 :::|||||||||
Db        915 ANCAAAAGGCTGGGC 929

RESULT 13
BQ057469
LOCUS       BQ057469                1058 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6739297 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813090
            5', mRNA sequence.
ACCESSION   BQ057469
VERSION     BQ057469.1  GI:19816809
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1058)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2064  row: j  column: 03
            High quality sequence stop: 631.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5813090"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_99"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

Alignment Scores:
Pred. No.:              1.18e-69        Length:         1058
Score:                  793.00          Matches:        157
Percent Similarity:     69.90%          Conservative:   59
Best Local Similarity:  50.81%          Mismatches:     85
Query Match:            27.45%          Indels:         9
DB:                     13              Gaps:           2

US-10-044-205A-2 (1-553) x BQ057469 (1-1058)

Qy        157 PheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeu 176
              :::|||         ||||||   |||::::::   |||   ::::::::::::||||||
Db         15 TACCTGAGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAACCGTTTCCTG 74

Qy        177 GlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgVal 196
              |||||||||      |||   |||||||||:::         |||   ::::::||||||
Db         75 CAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTC 134
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```
Qy        197 LeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMet 216
              |||||||||||||||||||||||||||||||||   ||||||:::   ||||||||||||
Db        135 CTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATG 194

Qy        217 TyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAla 236
              ||||||||||||||||||:::|||||||||:::||||||:::   ||||||   ||||||
Db        195 TATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCG 254

Qy        237 LeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyr 256
              |||   ||||||:::|||||||||||||||:::|||   |||:::|||||||||||||||
Db        255 CTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTAC 314

Qy        257 AlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeu 276
              |||:::|||:::|||      ||||||||||||::::::|||||||||||||||||||||
Db        315 GCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTC 374

Qy        277 LysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyr 296
              |||||||||||||||::::::|||      |||         :::|||   :::||||||
Db        375 AAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTAC 434

Qy        297 SerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAsp 316
              :::|||:::|||   ||||||:::      ||||||         |||||||||||||||
Db        435 GCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGAC 494

Qy        317 MetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGly 336
              :::||||||||||||:::||||||||||||   |||:::   |||:::||||||||||||
Db        495 CTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTCTGACCTGGGA 554

Qy        337 LeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyr 356
              |||||||||   :::      |||:::   |||      |||   ||||||   ||||||
Db        555 CTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTAC 614

Qy        357 MetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAla 376
              ||||||||||||::::::      :::      |||::::::      ||||||:::|||
Db        615 ATGGCTCCGGAGGTGGTGAAGAATGAA---CGGTACACGTTCAGCCCTGACTGGTGGGCG 671

Qy        377 MetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlu 396
              :::||||||   :::|||||||||:::|||   ::::::||||||:::      |||:::
Db        672 CTCGGCTGCCTCCTGTACGAGATGATCGCAAGCCAGTCGCCCTTCCAGCAGAGGAAGAAG 731

Qy        397 LysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHis 416
              |||:::   :::               |||      :::         :::
Db        732 AAGATCAAGCGGGG-ACGAGGTGGACCCGCTGGTGAAAGAAGTCCCCCAGGAGTATTCCG 790

Qy        417 AspAsnPheThrGluGluAlaLysAspIleCys-ArgLeuPheLeuAlaLysLysProGl 436
                    |||:::   :::|||:::   :::|||       ||||||   |||   |||
Db        791 AGCGCTTTTTCCCCGCAGGCCCGCTCACTTTGCTCACAGCTTCCTCTGCAAAGACCCTGC 850

Qy        436 uGlnArgLeuGlySerArgGluLysSerAspAspProArgLys----------------- 450
               :::|||||||||               :::   |||   |||
Db        851 CGAACGCCTGGGGGGGGTTCCGGGGGGCAACCGGCCCCCCAAGGTTGAAGGGAACCCCCC 910

Qy        451 -HisHisPhePheLysThrIleAsn 458
                     |||   |||::::::|||
Db        911 CCCTTCTTTTTAAAAAAGTGTAAAC 935

RESULT 14
BX392018/c
LOCUS       BX392018                 917 bp    mRNA    linear   EST 13-MAY-2003
DEFINITION  BX392018 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL010YD11 3-PRIME, mRNA sequence.
ACCESSION   BX392018
VERSION     BX392018.1  GI:30607809
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 917)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 3090.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAI046ZH12_CS04416_1&cluster=3090.f.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAI046ZH12_CS04416_1.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DL010YD11"
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                     /cell_line="RAMOS CELL LINE"
                     /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                     25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

Alignment Scores:
Pred. No.:                1.37e-69      Length:          917
Score:                    791.50        Matches:         149
Percent Similarity:       72.82%        Conservative:    60
Best Local Similarity:    51.92%        Mismatches:      71
Query Match:              27.40%        Indels:          7
DB:                       13            Gaps:            3

US-10-044-205A-2 (1-553) x BX392018 (1-917)

Qy        122 ProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu--- 140
              |||   |||   :::   :::   :::   |||   |||               :::
Db        891 CCTCATCCCTAAGTCCCCCGGCAGCTGGTGACGACCTGCACCCAGCGGCTGNAGCAGGGT 832

Qy        141 ------GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeu 158
                    ::::::            :::|||            |||         :::|||
Db        831 CCCTGCAAAGACCTTTTTCAGGAACTCACCCGGCTGACCCACGAG---------TACCTG 781

Qy        159 GlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrp 178
                       ||||||   |||::::::   |||   ::::::::::::||||||||||||
Db        780 AGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGG 721

Qy        179 LysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGly 198
              |||      |||   |||||||||:::         |||   ::::::||||||||||||
Db        720 AAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGC 661

Qy        199 LysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAla 218
              |||||||||||||||||||||||||||   ||||||:::   ||||||||||||||||||
Db        660 AAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCC 601

Qy        219 CysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeu 238
              ||||||||||||:::|||||||||:::||||||:::   ||||||   |||||||||
Db        600 TGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAAC 541

Qy        239 GluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPhe 258
              ||||||:::|||||||||||||||:::|||   |||:::||||||||||||||||||:::
Db        540 GAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTAT 481

Qy        259 GluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPhe 278
              |||:::|||      ||||||||||||::::::|||||||||||||||||||||||||||
Db        480 GAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTC 421

Qy        279 HisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAla 298
              |||||||||::::::|||      |||         :::|||   :::||||||:::|||
Db        420 CACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCC 361
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Qy          299 GlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLys 318
                :::|||   ||||||:::      ||||||         |||||||||||||||:::|||
Db          360 GAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAG 301

Qy          319 ProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAla 338
                |||||||||:::||||||||||||   |||:::   |||:::||||||||||||||||||
Db          300 CCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCT 241

Qy          339 ValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAla 358
                |||   :::      |||:::   |||      |||   ||||||   ||||||||||||
Db          240 GTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCT 181

Qy          359 ProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGly 378
                ||||||::::::      :::      |||::::::      ||||||:::|||:::|||
Db          180 CCGGAGGTGGTGAAGAATGAA---CGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGC 124

Qy          379 CysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysVal 398
                |||   :::|||||||||:::||||||::::::||||||:::      |||:::|||:::
Db          123 TGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATC 64

Qy          399 SerLysGluAspLeuLysGln 405
                   :::|||::::::::::::
Db           63 AAGCGGGAGGAGGTGGAGCGG 43

RESULT 15
BX849055
LOCUS       BX849055                 838 bp    mRNA    linear   EST 11-DEC-2003
DEFINITION  BX849055 Xenopus laevis oocyte Xenopus laevis cDNA clone
            IMAGp998G249027 ; IMAGE:3746735 5', mRNA sequence.
ACCESSION   BX849055
VERSION     BX849055.1  GI:39744402
KEYWORDS    EST.
SOURCE      Xenopus laevis (African clawed frog)
  ORGANISM  Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus.
REFERENCE   1  (bases 1 to 838)
  AUTHORS   Heil,O., Neubert,P., Peters,M., Radelof,U., Schneider,D.,
            Schroth,A., Korn,B. and Landgrebe,J.
  TITLE     Xenopus laevis UniGene Set 1 (RZPDLIB No.988)
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998G249027.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection (amp- resistant) (RZPDLIB
            No.998) http://www.rzpd.de/cgi-
            bin/products/showLib.pl.cgi/response?libNo=998 RZPDLIB; Xenopus
            laevis UniGene Set 1 (RZPDLIB No.988) http://www.rzpd.de/cgi-
            bin/products/showLib.pl.cgi/response?libNo=988 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            m13r, 5' TTTCACACAGGAAACAGCTATGAC 3'.
FEATURES             Location/Qualifiers
     source          1. .838
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="IMAGp998G249027 ; IMAGE:3746735"
                     /tissue_type="oocyte (stages 5 and 6)"
                     /lab_host="Top-10 F'"
                     /clone_lib="Xenopus laevis oocyte"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI; cDNA was prepared from 2ug of poly A+ RNA.
                     EcoRI-XhoI cut cDNA was then ligated into UniZap-XR
                     (Stratagene) with EcoRI at the 5' end and XhoI at the 3'
                     end. SS-library phagemids were prepared by mass excision
                     from the original library and normalized by hybridization
                     to biotinylated driver (prepared from the same library by
                     PCR) to Cot-omega of 11. After removal of hybrids and
                     excess driver by streptavidin sepharose chromatography,
                     the ss-phagemids were made double stranded and
                     electroporated into Top-10 F'. Original library
                     contruction by Bruce Blumberg (Blumberg et al., 1991
                     Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9,
                     2923-2935). Normalized by Jihwan Song (Song, Cho and
                     Blumberg, unpublished). Note: This is a Xenopus Gene
                     Collection (XGC) library."
ORIGIN

Alignment Scores:
Pred. No.:              3.48e-69        Length:         838
Score:                  787.00          Matches:        152
Percent Similarity:     71.18%          Conservative:   53
Best Local Similarity:  52.78%          Mismatches:     60
Query Match:            27.24%          Indels:         23
DB:                     13              Gaps:           4

US-10-044-205A-2 (1-553) x BX849055 (1-838)

Qy          121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
                ||||||            |||:::   :::   |||:::|||
Db           23 AATCCC------------AGCAAGGAAATATTCACTAGGTGC------------------ 52

Qy          141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
                                                 :::|||         ||||||
Db           53 ------------------------------ATTAGCGAACTCCATGAGTTCCTTAGTGGG 82

Qy          161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
                   ||||||:::::::::      |||   ::::::|||:::|||||||||||||||
Db           83 TCCCCGTTCCGAGAGTACCAGGAAAGTATGTACTTCGATCGTTTCTTGCAGTGGAAAAGC 142

Qy          181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
                   |||   |||   |||:::         |||   ::::::||||||||||||||||||
Db          143 CTAGAAAGACAACAGGTTACAAAAGATACTTTCCGGCAGTACAGGGTACTAGGCAAAGGT 202

Qy          201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
                |||||||||||||||||||||   ||||||:::   ||||||||||||||||||||||||
Db          203 GGCTTTGGGGAGGTGTGTGCGTGCCAAGTCCGTGCCACAGGGAAGATGTATGCTTGTAAA 262

Qy          221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
                ||||||:::|||||||||:::||||||:::   ||||||   |||||||||   ||||||
Db          263 AAACTAGAGAAGAAGAGGATCAAGAAGAGAAAGGGAGAATCAATGGCCCTGAATGAGAAG 322

Qy          241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
                :::|||||||||||||||:::|||   |||:::|||||||||||||||::::::|||:::
Db          323 CAGATCCTGGAGAAAGTGAACAGCCGTTTTGTGGTTAGTCTGGCTTACTCCTATGAAACG 382

Qy          261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
                |||      ||||||||||||:::::::::||||||||||||||||||||||||||||||
Db          383 AAAGACGCCCTGTGTCTGGTGCTGACGATCATGAACGGTGGTGACCTCAAGTTCCATATC 442

Qy          281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
                ||||||:::|||      |||   :::      ||||||:::||||||:::|||::::::
Db          443 TACAATATGGGAAATTCTGGCTTCGAGGAGGAACGTGTGGTCTTTTATGCTGCTGAGCTC 502

Qy          301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
                   ||||||:::   |||||||||:::   ||||||||||||||||||:::|||||||||
Db          503 TGCTGTGGCTTAGAACATCTACACCAGGAGGGAATTGTTTACAGGGATTTAAAACCAGAA 562

Qy          321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
                |||:::||||||||||||   |||:::   |||:::||||||||||||||||||::::::
Db          563 AATATCCTTTTGGATGATGATGGTCACATCAGGATATCAGACCTTGGTTTGGCAATCAAG 622

Qy          341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
                :::      |||      |||      |||   ||||||   ||||||||||||||||||
Db          623 ATACCAGAAGGGGACAGTATCCGGGGAAGAGTAGGCACAGTGGGTTATATGGCCCCAGAA 682

Qy          361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
                ::::::      :::      |||::::::      ||||||:::   :::||||||
Db        683 GTGATAAAGAATGAA---CGCTACACTTTTAGCCCGGACTGGTGGGGTTTGGGTTGTCTC 739

Qy        381 IleTyrGluMetVal-AlaGlyArgThrProPheLysAspTyrLysGluLysValSerLy 400
              ||||||||||||:::    |||      ||||||:::      ||||||:::|||   ||
Db        740 ATTTATGAGATGATCGAAGGGCCATCTTCCCTTTCGGCACGGGAAAGAACGAGTAAAAAA 799

Qy        400 s---GluAspLeuLysGlnArg 406
              |   :::   ||||||:::|||
Db        800 GGGAAAGAGGTTGAAAAAAAGG 821

Search completed: August 13, 2004, 21:10:27
Job time : 2727 secs
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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:         August 13, 2004, 18:45:41 ; Search time 92 Seconds
                                            (without alignments)
                                            3335.737 Million cell updates/sec

Title:          US-10-044-205A-2
Perfect score:  2889
Sequence:       1 MVDMGALDNLIANTAYLQAR.........NRPTGCEEGNSSKSGVCLLL 553

Scoring table:  BLOSUM62
                Xgapop 10.0 , Xgapext  0.5
                Ygapop 10.0 , Ygapext  0.5
                Fgapop  6.0 , Fgapext  7.0
                Delop   6.0 , Delext   7.0

Searched:       682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:      1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10044205_@CGN_1_1_54_@runat_06082004_104323_23382 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :      Issued_Patents_NA:*
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                5:  /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                          SUMMARIES
                 %
Result          Query
  No.   Score   Match Length DB  ID                   Description
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   2     2883    99.8   2249  4  US-09-802-117-5      Sequence 5, Appli
   3     2876    99.6   1662  4  US-09-738-894A-1     Sequence 1, Appli
   4     2876    99.6   1662  4  US-09-964-469-1      Sequence 1, Appli
   5     1801    62.3   1062  4  US-09-802-117-3      Sequence 3, Appli
   6     1528    52.9  36651  4  US-09-738-894A-3     Sequence 3, Appli
   7     1528    52.9  36651  4  US-09-964-469-3      Sequence 3, Appli
   8   1280.5    44.3   2113  4  US-09-614-748A-7     Sequence 7, Appli
   9   1252.5    43.4   2511  4  US-09-417-197-60     Sequence 60, Appl
  10   1252.5    43.4   2529  4  US-09-417-197-42     Sequence 42, Appl
  11   1252.5    43.4   2557  4  US-09-016-434-1298   Sequence 1298, Ap
  12   1250.5    43.3   1975  4  US-09-614-748A-9     Sequence 9, Appli
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  13   1243.5    43.0   2017  4  US-09-614-748A-8     Sequence 8, Appli
  14     1240    42.9   2848  3  US-08-464-954A-2     Sequence 2, Appli
  15     1238    42.9   2204  1  US-08-221-817-12     Sequence 12, Appl
  16     1238    42.9   2204  1  US-08-454-439-12     Sequence 12, Appl
  17     1238    42.9   2204  5  PCT-US94-10487-12    Sequence 12, Appl
  18   1236.5    42.8   2557  3  US-08-464-954A-1     Sequence 1, Appli
  19   1210.5    41.9   1879  4  US-09-614-748A-10    Sequence 10, Appl
  20   1210.5    41.9   1886  1  US-07-980-526-1      Sequence 1, Appli
  21   1209.5    41.9   2206  1  US-08-221-817-10     Sequence 10, Appl
  22   1209.5    41.9   2206  1  US-08-454-439-10     Sequence 10, Appl
  23   1209.5    41.9   2206  5  PCT-US94-10487-10    Sequence 10, Appl
  24     1189    41.2   1983  1  US-08-221-817-21     Sequence 21, Appl
  25     1189    41.2   1983  1  US-08-454-439-21     Sequence 21, Appl
  26     1189    41.2   1983  5  PCT-US94-10487-21    Sequence 21, Appl
  27   1023.5    35.4   1420  4  US-09-614-748A-11    Sequence 11, Appl
  28    991.5    34.3   1305  4  US-09-614-748A-12    Sequence 12, Appl
  29    725.5    25.1   2362  4  US-09-620-312D-273   Sequence 273, App
  30    721.5    25.0   2067  4  US-09-016-434-1306   Sequence 1306, Ap
  31      507    17.5   3255  4  US-09-016-434-1471   Sequence 1471, Ap
  32      493    17.1   2754  3  US-09-429-322-3      Sequence 3, Appli
  33    473.5    16.4   2274  4  US-09-772-647-3      Sequence 3, Appli
  34      469    16.2   2104  3  US-09-313-930-1      Sequence 1, Appli
  35      469    16.2   2104  4  US-09-023-655-1191   Sequence 1191, Ap
  36      469    16.2   2549  3  US-09-467-082-3      Sequence 3, Appli
  37      469    16.2   2549  4  US-09-394-455-5      Sequence 5, Appli
  38    466.5    16.1   1599  3  US-09-256-465-1      Sequence 1, Appli
  39    466.5    16.1   1599  4  US-09-167-322-3      Sequence 3, Appli
  40    466.5    16.1   1599  4  US-09-023-655-1004   Sequence 1004, Ap
  41      465    16.1   1788  4  US-09-417-197-68     Sequence 68, Appl
  42      461    16.0   2181  4  US-09-417-197-70     Sequence 70, Appl
  43      459    15.9   2968  4  US-08-685-852-1      Sequence 1, Appli
  44    458.5    15.9   2610  2  US-09-212-771-1      Sequence 1, Appli
  45    458.5    15.9   2610  3  US-09-091-058-1      Sequence 1, Appli


                               ALIGNMENTS

RESULT 1
US-09-802-117-1
; Sequence 1, Application US/09802117
; Patent No. 6444456
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/09/802,117
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER: US 60/188,449
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-802-117-1

Alignment Scores:
Pred. No.:              0               Length:         1662
Score:                  2883.00         Matches:        552
Percent Similarity:     99.82%          Conservative:   0
Best Local Similarity:  99.82%          Mismatches:     1
Query Match:            99.79%          Indels:         0
DB:                     4               Gaps:           0

US-10-044-205A-2 (1-553) x US-09-802-117-1 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
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Db          1 ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
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Qy           21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
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Db           61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy           41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy           61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy           81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy          101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
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Db          301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy          121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy          141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
                |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db          421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
                                              ala

Qy          161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy          181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy          201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy          221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy          241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy          261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy          281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy          301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy          321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy          341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy          361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy          381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy          401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy          421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy          441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
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Db         1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy          461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy          481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy          501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy          521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy          541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
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Db         1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 2
US-09-802-117-5
; Sequence 5, Application US/09802117
; Patent No. 6444456
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/09/802,117
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER: US 60/188,449
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 2249
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-802-117-5

Alignment Scores:
Pred. No.:                0              Length:         2249
Score:                    2883.00        Matches:        552
Percent Similarity:       99.82%         Conservative:   0
Best Local Similarity:    99.82%         Mismatches:     1
Query Match:              99.79%         Indels:         0
DB:                       4              Gaps:           0

US-10-044-205A-2 (1-553) x US-09-802-117-5 (1-2249)

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Qy          21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
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Db         414 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 473

Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         474 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 533

Qy          61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         534 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 593

Qy          81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
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Db         594 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 653

Qy         101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
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Db         654 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 713

Qy         121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         714 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 773

Qy         141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
               |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db         774 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 833

Qy         161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
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Db         834 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 893

Qy         181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
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Qy         201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
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Db         954 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 1013

Qy         221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
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Db        1014 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1073

Qy         241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
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Db        1074 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1133

Qy         261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
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Db        1134 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1193

Qy         281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
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Db        1194 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1253

Qy         301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
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Db        1254 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1313

Qy         321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
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Db        1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1373

Qy         341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
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Db        1374 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1433

Qy         361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1434 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1493

Qy         381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1494 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1553

Qy         401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1554 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1613

Qy         421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1614 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1673

Qy         441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1674 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1733

Qy         461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1734 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1793

Qy         481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1794 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1853

Qy         501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
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Db        1854 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1913

Qy         521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1914 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973

Qy         541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
               |||||||||||||||||||||||||||||||||||||||
Db        1974 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 2012

RESULT 3
US-09-738-894A-1
; Sequence 1, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636
;  CURRENT APPLICATION NUMBER: US/09/738,894A
;  CURRENT FILING DATE:  2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Human
US-09-738-894A-1

Alignment Scores:
Pred. No.:                0               Length:          1662
Score:                    2876.00         Matches:         551
Percent Similarity:       99.64%          Conservative:    0
Best Local Similarity:    99.64%          Mismatches:      2
Query Match:              99.55%          Indels:          0
DB:                       4               Gaps:            0

US-10-044-205A-2 (1-553) x US-09-738-894A-1 (1-1662)

Qy           1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy          21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
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Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 4
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV
;  CURRENT APPLICATION NUMBER: US/09/964,469
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Human
US-09-964-469-1

Alignment Scores:
Pred. No.:              0               Length:         1662
Score:                  2876.00         Matches:        551
Percent Similarity:     99.64%          Conservative:   0
Best Local Similarity:  99.64%          Mismatches:     2
Query Match:            99.55%          Indels:         0
DB:                     4               Gaps:           0

US-10-044-205A-2 (1-553) x US-09-964-469-1 (1-1662)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
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Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy          61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy          81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy         101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy         121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy         141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
               |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db         421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy         161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy         181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy         201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy         221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy         241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy         261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy         281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy         301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy         341 MetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAlaProGlu 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy         361 IleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGlyCysSer 380
               |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy         381 IleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysValSerLys 400
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy         401 GluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsnPheThr 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy         421 GluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArgLeuGly 440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy         441 SerArgGluLysSerAspAspProArgLysHisHisPhePheLysThrIleAsnPhePro 460
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy         461 ArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerValValTyrAla 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy         481 LysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPheAspAspLys 500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy         501 AspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrpGlnGluGlu 520
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy         521 IleIleGluThrGlyLeuPheGluGluLeuAsnAspProAsnArgProThrGlyCysGlu 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy         541 GluGlyAsnSerSerLysSerGlyValCysLeuLeuLeu 553
               |||||||||||||||||||||||||||||||||||||||
Db        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 5
US-09-802-117-3
; Sequence 3, Application US/09802117
; Patent No. 6444456
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/09/802,117
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER: US 60/188,449
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1062
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-802-117-3

Alignment Scores:
Pred. No.:                3.77e-202      Length:          1062
Score:                    1801.00        Matches:         349
Percent Similarity:       99.71%         Conservative:    0
Best Local Similarity:    99.71%         Mismatches:      1
Query Match:              62.34%         Indels:          0
DB:                       4              Gaps:            0

US-10-044-205A-2 (1-553) x US-09-802-117-3 (1-1062)

Qy           1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy          21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy          61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy          81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy         101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy         121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy         141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
                |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db         421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy         161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy         181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy         201 GlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAlaCysLys 220
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy         221 LysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeuGluLys 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy         241 GluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPheGluSer 260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy         261 LysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPheHisIle 280
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy         281 TyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAlaGlnIle 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy         301 AlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLysProGlu 320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         321 AsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAlaValGlu 340
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy         341 MetLysGlyGlyLysProIleThrGlnArg 350
                ||||||||||||||||||||||||||||||
Db        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1050

RESULT 6
US-09-738-894A-3
; Sequence 3, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636
;  CURRENT APPLICATION NUMBER: US/09/738,894A
;  CURRENT FILING DATE:  2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 36651
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(36651)
;   OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3

Alignment Scores:
Pred. No.:                  1.77e-167      Length:          36651
Score:                      1528.00        Matches:         349
Percent Similarity:         41.40%         Conservative:    0
Best Local Similarity:      41.40%         Mismatches:      1
Query Match:                52.89%         Indels:          493
DB:                         4              Gaps:            1

US-10-044-205A-2 (1-553) x US-09-738-894A-3 (1-36651)

Qy           1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2076 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 2135

Qy          21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2136 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 2195

Qy          41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2196 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 2255

Qy          61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2256 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 2315

Qy          81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2316 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 2375

Qy         101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2376 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 2435

Qy         121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2436 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 2495

Qy         141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
                |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db        2496 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 2555

Qy         161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2556 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 2615

Qy         181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2616 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 2675

Qy         201 GlyPheGlyGlu------------------------------------------------ 204
                ||||||||||||
Db        2676 GGTTTTGGGGAGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCATAGAGCATGA 2735

Qy         204 ------------------------------------------------------------ 204

Db        2736 AAGGGGGTAATGTTGCCTTTCTTTTTTAAATCTCAGTTACTTAGAACTAATTTCAGCAC 2795

Qy         204 ------------------------------------------------------------ 204
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Db       2796 CATATGTGGAGGATTTCTAGCCCCGTCTCCCCAGCCCCCTTCTTTGTGTGTGCCATGGTG 2855
Qy        204 ------------------------------------------------------------ 204
Db       2856 TGAAATAAAACACAAATGGCATGAGAGAGACAAGCAAAATTTATACTTGGCCAAGACTCT 2915
Qy        204 ------------------------------------------------------------ 204
Db       2916 GTCATGGGTCTCCATTAGGAACGTGCTGAGATGCCTGGACACTTCAGAGAATGATAGCAA 2975
Qy        204 ------------------------------------------------------------ 204
Db       2976 TGTGTGACAGAAGATCTCCGTTTCCCCTAAATTGTGATAATGAAGGCACTTCAAGAAAAA 3035
Qy        204 ------------------------------------------------------------ 204
Db       3036 TGGATATTTAAGAAAATACTCTAACTAGCTGGGTGTGGTGACATGCCTGTAATCCCAGCT 3095
Qy        204 ------------------------------------------------------------ 204
Db       3096 ACTTGGGAGGCTGAAGCAGGAGAATCACTTGAGCCTGGGAGGTGGAGGTTGCAGTGAGCC 3155
Qy        204 ------------------------------------------------------------ 204
Db       3156 AAGATCGTGCCACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCAAAAAAAAAAAAAAA 3215
Qy        204 ------------------------------------------------------------ 204
Db       3216 AAGAAAGAAAGAAAAGAAAGAAAACACTTATCTTGAAGTAAGGTTGAGAACCTGTTTTGT 3275
Qy        204 ------------------------------------------------------------ 204
Db       3276 ACCACTGTTGTGCCCAGCTTTCTGTTTTTAAGTAATAAAAAATATTTCAGGTAAAATTTG 3335
Qy        204 ------------------------------------------------------------ 204
Db       3336 CTTGATATAAAACTAACCATTAACTGTTTTAAAATGTACAATGCAGTGGCACTTCGCACA 3395
Qy        204 ------------------------------------------------------------ 204
Db       3396 AATGCAATGTTGGGTAAGCAACACCTCAATCTGGATCCAAGACACTCTCATCACCCCTGT 3455
Qy        204 ------------------------------------------------------------ 204
Db       3456 GCCCATTAATAGTGCCTCCCCATCCCTCTCCTCCTCCAGCCCTGACAACCACTAGTCCGC 3515
Qy        204 ------------------------------------------------------------ 204
Db       3516 TTTCTGTCTCTAGGGATTTGCCTATTCTGGGTGTTTCACACAATATGTGACCTTTTGTGT 3575
Qy        204 ------------------------------------------------------------ 204
Db       3576 CTGGCTTCTTTCACTCATTAGAATGTTTTTGGGGTTCATTCACACTGTAGCATGTGTCAA 3635
Qy        204 ------------------------------------------------------------ 204
Db       3636 TACTCCATTCCTTTTTATGGCTGTATAATATTCCATCGTATGGATGTACTACATTTCATG 3695
Qy        204 ------------------------------------------------------------ 204
Db       3696 TAGCCATTCATCTGTTGATGGACACTTGGGCTGTTTTCACCTTTTGGCTATTGTGTATGG 3755
Qy        204 ------------------------------------------------------------ 204
Db       3756 TGCTGCTATTCATGCACAAGTATTTGTTTGAATCCTTGTTTTCATTTCTCTTGGATTTAT 3815
Qy        204 ------------------------------------------------------------ 204
Db       3816 GCCCAGGAGTGGAATTGCTAGGGCATATGGTGATACTATGTTTAACTTTTCAAGGAGCCA 3875
Qy        204 ------------------------------------------------------------ 204

Db       3876 CCAAACTTTCCACATTTTTATTCCCACCAGCAATGCTTAAAGGTTTCGATTTCTCCACA 3935
Qy        204 ------------------------------------------------------------ 204
Db       3936 TCCTTGCCAACACTTGATATTTCCTGTATTTTTTATGAAGGCCTGCCTAGTGAGGTGA 3995
Qy        204 ------------------------------------------------------------ 204
Db       3996 AGGAGTATCGCACTGTAGTCCCCACTTTTTCTTGAGAACACTTCTTATTTACAGCTACTC 4055
Qy        204 ------------------------------------------------------------ 204
Db       4056 CTTTCTCCAATGCCTAACATCTTTCCACCCACCTCCTCCTTTATCATCTCCACCTCTCTG 4115
Qy        205 -------------------------------------------------ValCysAlaVa 208
                                                               |||||||||||
Db       4116 CAGTACCATCTACTTCTACCTCTTTCTCTTCTTTTCTTTCTCCTTTAAGGTATGTGCCGT 4175
Qy        208 lGlnValLysAsnThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLy 228
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4176 CCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAA 4235
Qy        228 sLysLysGlyGlyGluLysMetAlaLeuLeuGluLysGluIleLeuGluLysValSerSe 248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4236 GAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAG 4295
Qy        248 rProPheIleValSerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMe 268
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4296 CCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCAT 4355
Qy        268 tSerLeuMetAsnGlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLe 288
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4356 GAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCT 4415
Qy        288 uAspMetSerArgValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHi 308
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4416 GGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCA 4475
Qy        308 sGluLeuGlyIleValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGl 328
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4476 TGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGG 4535
Qy        328 yAsnCysArgLeuSerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleTh 348
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       4536 CAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCAC 4595
Qy        348 rGlnArg 350
              |||||||
Db       4596 CCAGAGG 4602

RESULT 7
US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV
;  CURRENT APPLICATION NUMBER: US/09/964,469
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 36651
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
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;    NAME/KEY: misc_feature
;    LOCATION: (1)...(36651)
;    OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

Alignment Scores:
Pred. No.:              1.77e-167     Length:        36651
Score:                  1528.00       Matches:       349
Percent Similarity:     41.40%        Conservative:  0
Best Local Similarity:  41.40%        Mismatches:    1
Query Match:            52.89%        Indels:        493
DB:                     4             Gaps:          1

US-10-044-205A-2 (1-553) x US-09-964-469-3 (1-36651)

Qy          1 MetValAspMetGlyAlaLeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArg 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2076 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 2135

Qy         21 LysProSerAspCysAspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuPro 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2136 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 2195

Qy         41 GlyLeuGlnGlyCysAlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCys 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2196 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 2255

Qy         61 GluGlnGlnProIleGlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPhe 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2256 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 2315

Qy         81 ArgLysAlaAlaThrPheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyPro 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2316 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 2375

Qy        101 ThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGly 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2376 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 2435

Qy        121 AsnProGlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2436 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 2495

Qy        141 GluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeuGlnGlu 160
              |||||||||||||||||||||||||||   ||||||||||||||||||||||||||||||
Db       2496 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 2555

Qy        161 GlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrpLysLeu 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2556 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 2615

Qy        181 PheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGlyLysGly 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2616 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 2675

Qy        201 GlyPheGlyGlu------------------------------------------------ 204
              ||||||||||||
Db       2676 GGTTTTGGGGAGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCATAGAGCATGA 2735

Qy        204 ------------------------------------------------------------ 204

Db       2736 AAGGGGGTAATGTTGCCTTTCTTTTTTTAAATCTCAGTTACTTAGAACTAATTTCAGCAC 2795

Qy        204 ------------------------------------------------------------ 204

Db       2796 CATATGTGGAGGATTTCTAGCCCCGTCTCCCCAGCCCCCTTCTTTGTGTGTGCCATGGTG 2855

Qy        204 ------------------------------------------------------------ 204

Db       2856 TGAAATAAAACACAAATGGCATGAGAGAGACAAGCAAAATTTATACTTGGCCAAGACTCT 2915

Qy        204 ------------------------------------------------------------ 204

Db       2916 GTCATGGGTCTCCATTAGGAACGTGCTGAGATGCCTGGACACTTCAGAGAATGATAGCAA 2975

Qy        204 ------------------------------------------------------------ 204

Db       2976 TGTGTGACAGAAGATCTCCGTTTCCCCTAAATTGTGATAATGAAGGCACTTCAAGAAAAA 3035

Qy        204 ------------------------------------------------------------ 204

Db       3036 TGGATATTTAAGAAAATACTCTAACTAGCTGGGTGTGGTGACATGCCTGTAATCCCAGCT 3095

Qy        204 ------------------------------------------------------------ 204

Db       3096 ACTTGGGAGGCTGAAGCAGGAGAATCACTTGAGCCTGGGAGGTGGAGGTTGCAGTGAGCC 3155

Qy        204 ------------------------------------------------------------ 204

Db       3156 AAGATCGTGCCACTGCACTCCAGCCTGGGTGACAGAGCAAGACTCAAAAAAAAAAAAAAA 3215

Qy        204 ------------------------------------------------------------ 204

Db       3216 AAGAAAGAAAGAAAAGAAAGAAAACACTTATCTTGAAGTAAGGTTGAGAACCTGTTTTGT 3275

Qy        204 ------------------------------------------------------------ 204

Db       3276 ACCACTGTTGTGCCCAGCTTTCTGTTTTTAAGTAATAAAAAATATTTCAGGTAAAATTTG 3335

Qy        204 ------------------------------------------------------------ 204

Db       3336 CTTGATATAAAACTAACCATTAACTGTTTTAAAATGTACAATGCAGTGGCACTTCGCACA 3395

Qy        204 ------------------------------------------------------------ 204

Db       3396 AATGCAATGTTGGGTAAGCAACACCTCAATCTGGATCCAAGACACTCTCATCACCCCTGT 3455

Qy        204 ------------------------------------------------------------ 204

Db       3456 GCCCATTAATAGTGCCTCCCCATCCCTCTCCTCCTCCAGCCCTGACAACCACTAGTCCGC 3515

Qy        204 ------------------------------------------------------------ 204

Db       3516 TTTCTGTCTCTAGGGATTTGCCTATTCTGGGTGTTTCACACAATATGTGACCTTTTGTGT 3575

Qy        204 ------------------------------------------------------------ 204

Db       3576 CTGGCTTCTTTCACTCATTAGAATGTTTTTGGGGTTCATTCACACTGTAGCATGTGTCAA 3635

Qy        204 ------------------------------------------------------------ 204

Db       3636 TACTCCATTCCTTTTTATGGCTGTATAATATTCCATCGTATGGATGTACTACATTTCATG 3695

Qy        204 ------------------------------------------------------------ 204

Db       3696 TAGCCATTCATCTGTTGATGGACACTTGGGCTGTTTTCACCTTTTGGCTATTGTGTATGG 3755

Qy        204 ------------------------------------------------------------ 204

Db       3756 TGCTGCTATTCATGCACAAGTATTTGTTTGAATCCTTGTTTTCATTTCTCTTGGATTTAT 3815

Qy        204 ------------------------------------------------------------ 204

Db       3816 GCCCAGGAGTGGAATTGCTAGGGCATATGGTGATACTATGTTTAACTTTTCAAGGAGCCA 3875

Qy        204 ------------------------------------------------------------ 204

Db       3876 CCAAACTTTCCACATTTTTTATTCCCACCAGCAATGCTTAAAGGTTTCGATTTCTCCACA 3935

Qy        204 ------------------------------------------------------------ 204

Db       3936 TCCTTGCCAACACTTGATATTTTCCTGTATTTTTTTATGAAGGCCTGCCTAGTGAGGTGA 3995

Qy        204 ------------------------------------------------------------ 204

Db       3996 AGGAGTATCGCACTGTAGTCCCCACTTTTTCTTGAGAACACTTCTTATTTACAGCTACTC 4055
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Qy       204 ------------------------------------------------------------ 204

Db      4056 CTTTCTCCAATGCCTAACATCTTTCCACCCACCTCCTCCTTTATCATCTCCACCTCTCTG 4115

Qy       205 -------------------------------------------------ValCysAlaVa 208
                                                              |||||||||||
Db      4116 CAGTACCATCTACTTCTACCTCTTTCTCTTCTTTTCTTTCTCCTTTAAGGTATGTGCCGT 4175

Qy       208 lGlnValLysAsnThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLy 228
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4176 CCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAA 4235

Qy       228 sLysLysGlyGlyGluLysMetAlaLeuLeuGluLysGluIleLeuGluLysValSerSe 248
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4236 GAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAG 4295

Qy       248 rProPheIleValSerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMe 268
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4296 CCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCAT 4355

Qy       268 tSerLeuMetAsnGlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLe 288
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4356 GAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCT 4415

Qy       288 uAspMetSerArgValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHi 308
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4416 GGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCA 4475

Qy       308 sGluLeuGlyIleValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGl 328
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4476 TGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGG 4535

Qy       328 yAsnCysArgLeuSerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleTh 348
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4536 CAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCAC 4595

Qy       348 rGlnArg 350
             |||||||
Db      4596 CCAGAGG 4602

RESULT 8
US-09-614-748A-7
; Sequence 7, Application US/09614748A
; Patent No. 6660474
; GENERAL INFORMATION:
;  APPLICANT: FELDER, ROBIN A.
;  APPLICANT:  JOSE, PEDRO
;  TITLE OF INVENTION: G PROTEIN-RELATED KINASE MUTANTS IN ESSENTIAL
;  TITLE OF INVENTION:  HYPERTENSION
;  FILE REFERENCE: FELDER 3.9-001 CONT
;  CURRENT APPLICATION NUMBER: US/09/614,748A
;  CURRENT FILING DATE:  2000-07-12
;  PRIOR APPLICATION NUMBER: PCT/US99/00663
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/071,199
;  PRIOR FILING DATE: 1998-01-12
;  PRIOR APPLICATION NUMBER: 60/098,279
;  PRIOR FILING DATE: 1998-08-28
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 2113
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-614-748A-7

Alignment Scores:
Pred. No.:              2.28e-140      Length:         2113
Score:                  1280.50        Matches:        254
Percent Similarity:     65.49%         Conservative:   97
Best Local Similarity:  47.39%         Mismatches:     162
Query Match:            44.32%         Indels:         23
DB:                     4              Gaps:           8

US-10-044-205A-2 (1-553) x US-09-614-748A-7 (1-2113)

Qy         7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSer---AspCys 25
             |||:::|||::::::||||||:::      |||:::||||||:::
Db       261 CTCGAGAACATCGTGGCCAACTCGCTGCTGCTGAAAGCGCGTCAAGGAGGATATGGCAAA 320

Qy        26 AspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
                |||         ::::::   :::      |||   ||||||   :::      |||
Db       321 AAAAGTGGTCGTAGTAAAAAATGGAAGGAGATACTGACACTGCCTCCTGTCAGCCAGTGC 380

Qy        46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
             :::|||||||||      :::      ::::::   |||||||||::::::|||||||||
Db       381 AGTGAGCTTAGACATTCCATTGAAAAGGATTATAGCAGTCTTTGTGACAAGCAACCGATA 440

Qy        66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
             ||||||||||||||||||   |||      |||   ||||||   ::::::
Db       441 GGAAGACGTCTCTTCAGGCAGTTCTGTGATACCAAACCCACTCTAAAGAGGCACATTGAA 500

Qy        86 PheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyProThrLysAsp------ 103
             ||||||:::   |||      :::|||:::|||::::::            |||
Db       501 TTCTTGGATGCAGTGGCAGAATATGAAGTTGCCGATGATGAGGACCGAAGTGATTGTGGA 560

Qy       104 ---SerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGlyAsnPro 122
                |||   |||                        :::||||||   |||      |||
Db       561 CTGTCAATCTTAGATAGATTCTTCAATGATAAGTTGGCAGCCCCTTTACCAGAAATACCT 620

Qy       123 GlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGluGluGlu 142
                                  |||   |||:::|||:::            ||||||
Db       621 CCAGAT---------------GTTGTGACAGAATGTAGATTGGGACTGAAGGAGGAGAAC 665

Qy       143 ArgValAlaAlaValThrLeuArgLysAla------------------GluAlaMetAla 156
                                  :::||||||                     |||
Db       666 ---------------CCTTCCAAAAAAGCCTTTGAGGAATGTACTAGAGTTGCCCATAAC 710

Qy       157 PheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeu 176
             :::|||:::   :::||||||:::::::::      |||:::::::::   :::||||||
Db       711 TACCTAAGAGGGGAACCATTTGAAGAATACCAAGAAAGCTCATATTTTTCTCAGTTTTTA 770

Qy       177 GlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgVal 196
             |||||||||      |||   |||||||||:::         |||      :::||||||
Db       771 CAATGGAAATGGCTGGAAAGGCAACCCGTAACAAAGAACACATTTAGACATTACAGAGTT 830

Qy       197 LeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMet 216
             |||||||||||||||||||||||||||||||||   ||||||:::   ||||||||||||
Db       831 CTAGGAAAAGGCGGATTTGGAGAGGTTTGCGCCTGTCAAGTGCGAGCCACAGGAAAAATG 890

Qy       217 TyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAla 236
             ||||||||||||||||||   |||||||||:::||||||:::   ||||||   ||||||
Db       891 TATGCCTGCAAAAAGCTACAAAAAAAAAGAATAAAGAAGAGGAAAGGTGAAGCTATGGCT 950

Qy       237 LeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyr 256
             |||   ||||||   |||||||||||||||   |||   |||:::|||||||||||||||
Db       951 CTAAATGAGAAAAGAATTCTGGAGAAAGTGCAAAGTAGATTCGTAGTTAGTTTAGCCTAC 1010

Qy       257 AlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeu 276
             |||:::|||:::|||      ||||||||||||:::::::::||||||||||||||||||
Db      1011 GCTTATGAAACCAAAGATGCCTTGTGCTTGGTGCTCACCATTATGAATGGAGGGGATTTG 1070

Qy       277 LysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyr 296
             ||||||||||||||||||:::|||      |||   |||      |||   :::||||||
Db      1071 AAGTTTCACATTTACAACCTGGGCAATCCCGGCTTTGATGAGCAGAGAGCCGTTTTCTAT 1130

Qy       297 SerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAsp 316
             :::|||::::::   ||||||:::      |||            |||||||||||||||
Db      1131 GCTGCAGAGCTGTGTTGCGGCTTGGAAGATTTACAGAGGGAAAGAATTGTATACAGAGAC 1190

Qy       317 MetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGly 336
             :::||||||||||||:::||||||||||||   |||:::   |||:::||||||||||||
Db      1191 TTGAAGCCTGAGAATATTCTCCTTGATGATCGTGGACACATCCGGATTTCAGACCTCGGT 1250

Qy       337 LeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyr 356
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             ||||||   |||:::      |||:::   :::      |||   ||||||   ||||||
Db      1251 TTGGCCACAGAGATCCCAGAAGGACAGAGGGTTCGAGGAAGAGTTGGAACAGTCGGCTAC 1310

Qy       357 MetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAla 376
             ||||||||||||::::::      :::      |||::::::      ||||||:::
Db      1311 ATGGCACCTGAAGTTGTCAATAATGAA---AAGTATACGTTTAGTCCCGATTGGTGGGGA 1367

Qy       377 MetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlu 396
             :::||||||   ||||||||||||:::   |||   :::|||||||||   |||||||||
Db      1368 CTTGGCTGTCTGATCTATGAAATGATTCAGGGACATTCTCCATTCAAAAAATACAAAGAG 1427

Qy       397 LysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHis 416
             ||||||      |||::::::   ||||||         |||      ::::::
Db      1428 AAAGTCAAATGGAGGAGGTCGATCAAAGAATCAAGAATGATACCGAGGAGTATTCT--- 1484

Qy       417 AspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGlu 436
             :::   |||:::|||:::||||||   |||||||||:::   |||   |||   |||
Db      1485 GAGAAGTTTTCAGAGGATGCCAAATCTATCTGCAGGATGTTACTCACCAAGAATCCAAGC 1544

Qy       437 GlnArgLeuGlySerArg---GluLysSerAspAspProArgLysHisHisPhePheLys 455
             :::|||:::|||   |||   |||   :::         ::::::|||      ||||||
Db      1545 AAGCGGGTGGGCTGCAGGGGCGAGGGAGCGGCTGGGGTGAAGCAGCACCCCGTGTTCAAG 1604

Qy       456 ThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAspPro 475
                |||||||||   ||||||||||||   ::::::||||||||||||   |||||||||
Db      1605 GACATCAACTTCAGGAGGCTGGAGGCAAACATGCTGGAGCCCCCTTTCTGTCCTGATCCT 1664

Qy       476 SerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGlyVal 495
                   ||||||   ||||||:::   :::|||:::   ||||||   |||:::|||:::
Db      1665 CATGCCGTTTACTGTAAGGACGTCCTGGATATCGAGCAGTTCTCGGCGGTGAAAGGGATC 1724

Qy       496 GluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIle 515
                   |||      |||:::   |||:::      ||||||||||||   |||   |||
Db      1725 TACCTGGACACCGCAGATGAAGACTTCTATGCTCGGTTTGCTACCGGGTGTGTCTCCATC 1784

Qy       516 AlaTrpGlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
                ||||||   |||:::||||||:::|||   |||:::::::::|||
Db      1785 CCCTGGCAGAATGAGATGATCGAATCCGGGTGTTTCAAAGACATCAAC 1832

RESULT 9
US-09-417-197-60
; Sequence 60, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
;  APPLICANT: Ole THASTRUP, et al.
;  TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
;  TITLE OF INVENTION:  On A Cellular Response
;  FILE REFERENCE: 3759-0110P
;  CURRENT APPLICATION NUMBER: US/09/417,197
;  CURRENT FILING DATE:  1999-10-07
;  NUMBER OF SEQ ID NOS: 143
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 60
;   LENGTH: 2511
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Grk5-EGFP fusion
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2508)
US-09-417-197-60

 Alignment Scores:
 Pred. No.:              6e-137         Length:         2511
 Score:                  1252.50        Matches:        259
 Percent Similarity:     63.07%         Conservative:   103
 Best Local Similarity:  45.12%         Mismatches:     162
 Query Match:            43.35%         Indels:         50
 DB:                     4              Gaps:           11

 US-10-044-205A-2 (1-553) x US-09-417-197-60 (1-2511)
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Qy         7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSerAspCysAsp 26
             |||:::|||::::::|||||||||      |||:::||||||:::
Db         7 CTGGAAAACATCGTGGCCAACACGGTCTTGCTGAAAGCCAGGGAAGGGGGCGGAGGAAAG 66

Qy        27 SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
                |||         ::::::   :::      |||      |||   :::      |||
Db        67 CGCAAAGGGAAAAGCAAGAAGTGGAAAGAAATCCTGAAGTTCCCTCACATTAGCCAGTGT 126

Qy        46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
                :::||||||:::   :::      ::::::   |||||||||::::::|||||||||
Db       127 GAAGACCTCCGAAGGACCATAGACAGAGATTACTGCAGTTTATGTGACAAGCAGCCAATC 186

Qy        66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
             ||||||   |||||||||   |||      |||   |||
Db       187 GGGAGGCTGCTTTTCCGGCAGTTTTGTGAAACCAGGCCTGGGCTGGAGTGTTACATTCAG 246

Qy        86 PheLeuGluAspValGlnAsnTrpGlu------------------LeuAlaGluGluGly 99
             ||||||:::   |||      :::|||                  |||   |||:::|||
Db       247 TTCCTGGACTCCGTGGCAGAATATGAAGTTACTCCAGATGAAAAACTGGGAGAGAAAGGG 306

Qy       100 ProThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaPro 119
                   |||:::         :::   |||                           |||
Db       307 ------AAGGAAATTATGACCAAGTACCTC------------------------ACCCCA 336

Qy       120 GlyAsnPro---------------------GlnProPheLeuSerGlnAlaValAlaThr 132
                :::|||                     |||      :::||||||
Db       337 AAGTCCCCTGTTTTCATAGCCCAAGTTGGCCAAGACCTGGTCTCCCAGACGGAGGAGAAG 396

Qy       133 LysCysGlnAlaAlaThrThrGluGluGluArgValAlaAlaValThrLeuArgLysAla 152
                   |||            |||               |||   ::::::   :::
Db       397 CTCCTACAGAAGCCGTGCAAAGAACTCTTTTCTGCCTGTGCACAGTCTGTCCACGAG--- 453

Qy       153 GluAlaMetAlaPheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyr 172
                         :::|||:::   :::||||||   :::::::::   |||   |||:::
Db       454 ------------TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTT 501

Qy       173 AspLysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThr 192
             |||:::|||||||||||||||      |||   |||||||||:::         |||
Db       502 GACCGCTTTCTCCAGTGGAAGTGGTTGGAAAGGCAACCGGTGACCAAAAACACTTTCAGG 561

Qy       193 GluPheArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsn 212
             ::::::|||||||||||||||||||||||||||||||||||||||   ||||||:::
Db       562 CAGTATCGAGTGCTAGGAAAAGGGGGCTTCGGGGAGGTCTGTGCCTGCCAGGTTCGGGCC 621

Qy       213 ThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGly 232
             ||||||||||||||||||||||||:::|||:::|||||||||:::||||||:::   |||
Db       622 ACGGGTAAAATGTATGCCTGCAAGCGCTTGGAGAAGAAGAGGATCAAAAAGAGGAAAGGG 681

Qy       233 GluLysMetAlaLeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleVal 252
             |||   |||||||||   ||||||:::|||||||||||||||:::|||   |||:::|||
Db       682 GAGTCCATGGCCCTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTC 741

Qy       253 SerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsn 272
             :::||||||||||||:::|||:::|||      ||||||||||||:::::::::||||||
Db       742 AACCTGGCCTATGCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAAT 801

Qy       273 GlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArg 292
             ||||||||||||||||||||||||||||||:::|||      |||   :::      |||
Db       802 GGGGGTGACCTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGG 861

Qy       293 ValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIle 312
                :::||||||:::|||:::|||   ||||||:::      ||||||
Db       862 GCCTTGTTTTATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACC 921

Qy       313 ValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeu 332
             ||||||||||||:::||||||||||||:::||||||||||||   |||:::   |||:::
Db       922 GTCTACCGAGATCTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATC 981

Qy       333 SerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGly 352
             |||||||||||||||||||||::::::      |||      |||      |||   |||
Db       982 TCAGACCTGGGCTTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGC 1041

Qy       353 ThrAsnGlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProVal 372
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               |||   ||||||||||||||||||:::|||      :::      |||
Db        1042 ACTGTTGGCTACATGGCCCCCGAAGTCCTGAACAACCAG---AGGTACGGCCTGAGCCCC 1098

Qy         373 AspTrpPheAlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLys 392
               |||::::::   :::||||||   ||||||||||||:::   |||::::::||||||:::
Db        1099 GACTACTGGGGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGC 1158

Qy         393 AspTyrLysGluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluVal 412
                     ||||||||||||   :::|||::::::   :::|||   |||:::   |||
Db        1159 GGCCGTAAGGAGAAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGGAGGAG 1218

Qy         413 LysPheGlnHisAspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAla 432
                  :::   |||      |||:::||||||||||||   ||||||::::::   |||
Db        1219 GTGTACTCCCAC---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACG 1275

Qy         433 LysLysProGluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHis 451
               |||      :::||||||||||||   :::|||:::   :::   :::   ::::::|||
Db        1276 AAAGATGCGAAGCAGAGGCTGGGCTGCCAGGAGGAGGGGGCTGCAGAGGTCAAGAGACAC 1335

Qy         452 HisPhePheLysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPhe 471
                  ||||||:::   :::||||||   |||||||||||||||:::::::::|||||||||
Db        1336 CCCTTCTTCAGGAACATGAACTTCAAGCGCTTAGAAGCCGGGATGTTGGACCCTCCCTTC 1395

Qy         472 ValProAspProSerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGlu 491
               ||||||||||||      ||||||   ||||||:::   :::|||:::   ||||||
Db        1396 GTTCCAGACCCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACT 1455

Qy         492 ValArgGlyValGluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGly 511
               |||:::||||||      |||      |||      |||:::      |||:::||||||
Db        1456 GTGAAGGGCGTCAATCTGGACCACACAGACGACGACTTCTACTCCAAGTTCTCCACGGGC 1515

Qy         512 AlaValProIleAlaTrpGlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
               :::|||   |||   ||||||   |||:::|||||||||      |||:::|||||||||
Db        1516 TCTGTGTCCATCCCATGGCAAAACGAGATGATAGAAACAGAATGCTTTAAGGAGCTGAAC 1575

Qy         532 ------------------------------------------------AspPro-AsnAr 535
                                                               |||    |||||
Db        1576 GTGTTTGGACCTAATGGTACCCTCCCGCCAGATCTGAACAGAAACCACCCTCCGGAACCG 1635

Qy         535 gPro---ThrGlyCysGluGluGlyAsnSerSerLysSer 547
               ||||      ||||||         :::||||||   |||
Db        1636 CCCAAGAAAGGGCTGCTCCAGAGACTCTTCAAGCGGCAGC 1675

RESULT 10
US-09-417-197-42
; Sequence 42, Application US/09417197
; Patent No. 6518021
; GENERAL INFORMATION:
;  APPLICANT: Ole THASTRUP, et al.
;  TITLE OF INVENTION: A Method For Extracting Quantitative Information Relating To An I
;  TITLE OF INVENTION:  On A Cellular Response
;  FILE REFERENCE: 3759-0110P
;  CURRENT APPLICATION NUMBER: US/09/417,197
;  CURRENT FILING DATE:  1999-10-07
;  NUMBER OF SEQ ID NOS: 143
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
;   LENGTH: 2529
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: EGFP-Grk5 fusion
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2526)
US-09-417-197-42

Alignment Scores:
Pred. No.:               6.08e-137      Length:          2529
Score:                   1252.50        Matches:         259
Percent Similarity:      63.07%         Conservative:    103
Best Local Similarity:   45.12%         Mismatches:      162
Query Match:             43.35%         Indels:          50
DB:                      4              Gaps:            11

US-10-044-205A-2 (1-553) x US-09-417-197-42 (1-2529)

Qy           7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSerAspCysAsp 26
               |||:::|||::::::|||||||||      |||:::||||||:::
Db         763 CTGGAAAACATCGTGGCCAACACGGTCTTGCTGAAAGCCAGGGAAGGGGGCGGAGGAAAG 822

Qy          27 SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
                  |||         ::::::   :::      |||      |||   :::      |||
Db         823 CGCAAAGGGAAAAGCAAGAAGTGGAAAGAAATCCTGAAGTTCCCTCACATTAGCCAGTGT 882

Qy          46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
                  :::||||||:::   :::      ::::::   |||||||||::::::|||||||||
Db         883 GAAGACCTCCGAAGGACCATAGACAGAGATTACTGCAGTTTATGTGACAAGCAGCCAATC 942

Qy          66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
               ||||||   |||||||||   |||      |||   |||
Db         943 GGGAGGCTGCTTTTCCGGCAGTTTTGTGAAACCAGGCCTGGGCTGGAGTGTTACATTCAG 1002

Qy          86 PheLeuGluAspValGlnAsnTrpGlu------------------LeuAlaGluGluGly 99
               ||||||:::   |||      :::|||                  |||   |||:::|||
Db        1003 TTCCTGGACTCCGTGGCAGAATATGAAGTTACTCCAGATGAAAAACTGGGAGAGAAAGGG 1062

Qy         100 ProThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaPro 119
                     |||:::         :::   |||                           |||
Db        1063 ------AAGGAAATTATGACCAAGTACCTC------------------------ACCCCA 1092

Qy         120 GlyAsnPro---------------------GlnProPheLeuSerGlnAlaValAlaThr 132
                  :::|||                     |||      :::||||||
Db        1093 AAGTCCCCTGTTTTCATAGCCCAAGTTGGCCAAGACCTGGTCTCCCAGACGGAGGAGAAG 1152

Qy         133 LysCysGlnAlaAlaThrThrGluGluGluArgValAlaAlaValThrLeuArgLysAla 152
                     |||            |||               |||   ::::::   :::
Db        1153 CTCCTACAGAAGCCGTGCAAAGAACTCTTTTCTGCCTGTGCACAGTCTGTCCACGAG--- 1209

Qy         153 GluAlaMetAlaPheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyr 172
                           :::|||:::   :::||||||   :::::::::   |||   |||:::
Db        1210 ------------TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTT 1257

Qy         173 AspLysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThr 192
               |||:::|||||||||||||||      |||   |||||||||:::         |||
Db        1258 GACCGCTTTCTCCAGTGGAAGTGGTTGGAAAGGCAACCGGTGACCAAAAACACTTTCAGG 1317

Qy         193 GluPheArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsn 212
               ::::::|||||||||||||||||||||||||||||||||||||||   ||||||:::
Db        1318 CAGTATCGAGTGCTAGGAAAAGGGGGCTTCGGGGAGGTCTGTGCCTGCCAGGTTCGGGCC 1377

Qy         213 ThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGly 232
               ||||||||||||||||||||||||:::|||:::|||||||||:::||||||:::   |||
Db        1378 ACGGGTAAAATGTATGCCTGCAAGCGCTTGGAGAAGAAGAGGATCAAAAAGAGGAAAGGG 1437

Qy         233 GluLysMetAlaLeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleVal 252
               |||   |||||||||   ||||||:::|||||||||||||||:::|||   |||:::|||
Db        1438 GAGTCCATGGCCCTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTC 1497

Qy         253 SerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsn 272
               :::||||||||||||:::|||:::|||      ||||||||||||:::::::::||||||
Db        1498 AACCTGGCCTATGCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAAT 1557

Qy         273 GlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArg 292
               ||||||||||||||||||||||||||||||:::|||      |||   :::      |||
Db        1558 GGGGGTGACCTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGG 1617

Qy         293 ValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIle 312
                  :::||||||:::|||:::|||   ||||||:::      ||||||
Db        1618 GCCTTGTTTTATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACC 1677

Qy         313 ValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeu 332
               ||||||||||||:::||||||||||||:::||||||||||||   |||:::   |||:::
Db        1678 GTCTACCGAGATCTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATC 1737

Qy         333 SerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGly 352
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              |||||||||||||||||||||::::::      |||      |||      |||   |||
Db       1738 TCAGACCTGGGCTTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGC 1797

Qy        353 ThrAsnGlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProVal 372
              |||   ||||||||||||||||||:::|||      :::      |||
Db       1798 ACTGTTGGCTACATGGCCCCCGAAGTCCTGAACAACCAG---AGGTACGGCCTGAGCCCC 1854

Qy        373 AspTrpPheAlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLys 392
              |||::::::   :::||||||   ||||||||||||:::   |||::::::||||||:::
Db       1855 GACTACTGGGGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGC 1914

Qy        393 AspTyrLysGluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluVal 412
                    ||||||||||||   :::|||::::::   :::|||   |||:::   |||
Db       1915 GGCCGTAAGGAGAAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGGAGGAG 1974

Qy        413 LysPheGlnHisAspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAla 432
                 :::   |||      |||:::||||||||||||   ||||||::::::   |||
Db       1975 GTGTACTCCCAC---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACG 2031

Qy        433 LysLysProGluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHis 451
              |||      :::||||||||||||   :::|||:::   :::   :::   ::::::|||
Db       2032 AAAGATGCGAAGCAGAGGCTGGGCTGCCAGGAGGAGGGGGCTGCAGAGGTCAAGAGACAC 2091

Qy        452 HisPhePheLysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPhe 471
                 ||||||:::   :::||||||   |||||||||||||||:::::::::|||||||||
Db       2092 CCCTTCTTCAGGAACATGAACTTCAAGCGCTTAGAAGCCGGGATGTTGGACCCTCCCTTC 2151

Qy        472 ValProAspProSerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGlu 491
              ||||||||||||      ||||||   ||||||:::   :::|||:::   ||||||
Db       2152 GTTCCAGACCCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACT 2211

Qy        492 ValArgGlyValGluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGly 511
              |||:::||||||      |||      |||      |||:::      |||:::||||||
Db       2212 GTGAAGGGCGTCAATCTGGACCACACAGACGACGACTTCTACTCCAAGTTCTCCACGGGC 2271

Qy        512 AlaValProIleAlaTrpGlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
              :::|||   |||   ||||||   |||:::|||||||||      |||:::|||||||||
Db       2272 TCTGTGTCCATCCCATGGCAAAACGAGATGATAGAAACAGAATGCTTTAAGGAGCTGAAC 2331

Qy        532 ------------------------------------------------AspPro-AsnAr 535
                                                                 ||| |||||
Db       2332 GTGTTTGGACCTAATGGTACCCTCCCGCCAGATCTGAACAGAAACCACCCTCCGGAACCG 2391

Qy        535 gPro---ThrGlyCysGluGluGlyAsnSerSerLysSer 547
              ||||      ||||||         :::||||||   |||
Db       2392 CCCAAGAAAGGGCTGCTCCAGAGACTCTTCAAGCGGCAGC 2431

RESULT 11
US-09-016-434-1298
; Sequence 1298, Application US/09016434
; Patent No. 6500938
;  GENERAL INFORMATION:
;    APPLICANT:  Janice Au-Young
;    APPLICANT:  Jeffrey J. Seilhamer
;    TITLE OF INVENTION:  COMPOSITION FOR THE DETECTION OF SIGNALING
;    TITLE OF INVENTION:  PATHWAY GENE EXPRESSION
;    NUMBER OF SEQUENCES:  1490
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  INCYTE PHARMACEUTICALS, INC.
;      STREET:  3174 PORTER DRIVE
;      CITY:  PALO ALTO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/016,434
;      FILING DATE:  HEREWITH
;      CLASSIFICATION:
```

```
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Zeller, Karen J.
;      REGISTRATION NUMBER:  37,071
;      REFERENCE/DOCKET NUMBER:  PA-0002 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 855-0555
;      TELEFAX:  (650) 845-4166
;  INFORMATION FOR SEQ ID NO:  1298:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2557 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GENBANK
;      CLONE:  g306804
US-09-016-434-1298

Alignment Scores:
Pred. No.:              6.19e-137     Length:         2557
Score:                  1252.50       Matches:        259
Percent Similarity:     63.07%        Conservative:   103
Best Local Similarity:  45.12%        Mismatches:     162
Query Match:            43.35%        Indels:         50
DB:                     4             Gaps:           11

US-10-044-205A-2 (1-553) x US-09-016-434-1298 (1-2557)

Qy          7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSerAspCysAsp 26
              |||:::|||::::::|||||||||      |||:::||||||:::
Db        227 CTGGAAAACATCGTGGCCAACACGGTCTTGCTGAAAGCCAGGGAAGGGGGCGGAGGAAAG 286

Qy         27 SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
                 |||         ::::::   :::      |||      |||   :::      |||
Db        287 CGCAAAGGGAAAAGCAAGAAGTGGAAAGAAATCCTGAAGTTCCCTCACATTAGCCAGTGT 346

Qy         46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
                 :::||||||:::   :::      ::::::   |||||||||::::::|||||||||
Db        347 GAAGACCTCCGAAGGACCATAGACAGAGATTACTGCAGTTTATGTGACAAGCAGCCAATC 406

Qy         66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
              ||||||   |||||||||   |||      |||   |||
Db        407 GGGAGGCTGCTTTTCCGGCAGTTTTGTGAAACCAGGCCTGGGCTGGAGTGTTACATTCAG 466

Qy         86 PheLeuGluAspValGlnAsnTrpGlu------------------LeuAlaGluGluGly 99
              ||||||:::   |||      :::|||                  |||   |||:::|||
Db        467 TTCCTGGACTCCGTGGCAGAATATGAAGTTACTCCAGATGAAAAACTGGGAGAGAAAGGG 526

Qy        100 ProThrLysAspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaPro 119
                    |||:::         :::   |||                           |||
Db        527 ------AAGGAAATTATGACCAAGTACCTC------------------------ACCCCA 556

Qy        120 GlyAsnPro---------------------GlnProPheLeuSerGlnAlaValAlaThr 132
                 :::|||                     |||      :::||||||
Db        557 AAGTCCCCTGTTTTCATAGCCCAAGTTGGCCAAGACCTGGTCTCCCAGACGGAGGAGAAG 616

Qy        133 LysCysGlnAlaAlaThrThrGluGluGluArgValAlaAlaValThrLeuArgLysAla 152
                    |||            |||               |||   ::::::   :::
Db        617 CTCCTACAGAAGCCGTGCAAAGAACTCTTTTCTGCCTGTGCACAGTCTGTCCACGAG--- 673

Qy        153 GluAlaMetAlaPheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyr 172
                          :::|||:::   :::||||||   :::::::::   |||   |||:::
Db        674 ------------TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTT 721

Qy        173 AspLysPheLeuGlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThr 192
              |||:::|||||||||||||||      |||   |||||||||:::         |||
Db        722 GACCGCTTTCTCCAGTGGAAGTGGTTGGAAAGGCAACCGGTGACCAAAAACACTTTCAGG 781

Qy        193 GluPheArgValLeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsn 212
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              ::::::|||||||||||||||||||||||||||||||||||||||   ||||||:::
Db        782 CAGTATCGAGTGCTAGGAAAAGGGGGCTTCGGGGAGGTCTGTGCCTGCCAGGTTCGGGCC 841

Qy        213 ThrGlyLysMetTyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGly 232
              ||||||||||||||||||||||||:::|||:::|||||||||:::||||||:::   |||
Db        842 ACGGGTAAAATGTATGCCTGCAAGCGCTTGGAGAAGAAGAGGATCAAAAAGAGGAAAGGG 901

Qy        233 GluLysMetAlaLeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleVal 252
              |||   |||||||||   ||||||:::|||||||||||||||:::|||   |||:::|||
Db        902 GAGTCCATGGCCCTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTC 961

Qy        253 SerLeuAlaTyrAlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsn 272
              :::||||||||||||:::|||:::|||      ||||||||||||:::::::::||||||
Db        962 AACCTGGCCTATGCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAAT 1021

Qy        273 GlyGlyAspLeuLysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArg 292
              ||||||||||||||||||||||||||||||:::|||      |||   :::      |||
Db       1022 GGGGGTGACCTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGG 1081

Qy        293 ValIlePheTyrSerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIle 312
                 :::||||||:::|||:::|||   ||||||:::      ||||||
Db       1082 GCCTTGTTTTATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACC 1141

Qy        313 ValTyrArgAspMetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeu 332
              ||||||||||||:::||||||||||||:::||||||||||||   |||:::   |||:::
Db       1142 GTCTACCGAGATCTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATC 1201

Qy        333 SerAspLeuGlyLeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGly 352
              |||||||||||||||||||||::::::      |||      |||      |||   |||
Db       1202 TCAGACCTGGGCTTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGC 1261

Qy        353 ThrAsnGlyTyrMetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProVal 372
              |||   ||||||||||||||||||:::|||      :::      |||
Db       1262 ACTGTTGGCTACATGGCCCCCGAAGTCCTGAACAACCAG---AGGTACGGCCTGAGCCCC 1318

Qy        373 AspTrpPheAlaMetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLys 392
              |||::::::   :::||||||   ||||||||||||:::   |||::::::||||||:::
Db       1319 GACTACTGGGGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGC 1378

Qy        393 AspTyrLysGluLysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluVal 412
                    ||||||||||||   :::|||::::::   :::|||   |||:::   |||
Db       1379 GGCCGTAAGGAGAAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGGAGGAG 1438

Qy        413 LysPheGlnHisAspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAla 432
                 :::   |||      |||:::||||||||||||   ||||||::::::   |||
Db       1439 GTGTACTCCCAC---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACG 1495

Qy        433 LysLysProGluGlnArgLeuGlySerArgGluLys---SerAspAspProArgLysHis 451
              |||      :::||||||||||||   :::|||:::   :::   :::   ::::::|||
Db       1496 AAAGATGCGAAGCAGAGGCTGGGCTGCCAGGAGGAGGGGGCTGCAGAGGTCAAGAGACAC 1555

Qy        452 HisPhePheLysThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPhe 471
                 ||||||:::   :::||||||   |||||||||||||||:::::::::|||||||||
Db       1556 CCCTTCTTCAGGAACATGAACTTCAAGCGCTTAGAAGCCGGGATGTTGGACCCTCCCTTC 1615

Qy        472 ValProAspProSerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGlu 491
              ||||||||||||      ||||||   ||||||:::   :::|||:::   ||||||
Db       1616 GTTCCAGACCCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACT 1675

Qy        492 ValArgGlyValGluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGly 511
              |||:::||||||      |||      |||      |||:::      |||:::||||||
Db       1676 GTGAAGGGCGTCAATCTGGACCACACAGACGACGACTTCTACTCCAAGTTCTCCACGGGC 1735

Qy        512 AlaValProIleAlaTrpGlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
              :::|||   |||   ||||||   |||:::|||||||||      |||:::|||||||||
Db       1736 TCTGTGTCCATCCCATGGCAAAACGAGATGATAGAAACAGAATGCTTTAAGGAGCTGAAC 1795

Qy        532 ------------------------------------------------AspPro-AsnAr 535
                                                                 ||| |||||
Db       1796 GTGTTTGGACCTAATGGTACCCTCCCGCCAGATCTGAACAGAAACCACCCTCCGGAACCG 1855

Qy        535 gPro---ThrGlyCysGluGluGlyAsnSerSerLysSer 547
              ||||      ||||||         :::||||||   |||
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Db       1856 CCCAAGAAAGGGCTGCTCCAGAGACTCTTCAAGCGGCAGC 1895

RESULT 12
US-09-614-748A-9
; Sequence 9, Application US/09614748A
; Patent No. 6660474
; GENERAL INFORMATION:
;  APPLICANT: FELDER, ROBIN A.
;  APPLICANT:  JOSE, PEDRO
;  TITLE OF INVENTION: G PROTEIN-RELATED KINASE MUTANTS IN ESSENTIAL
;  TITLE OF INVENTION:  HYPERTENSION
;  FILE REFERENCE: FELDER 3.9-001 CONT
;  CURRENT APPLICATION NUMBER: US/09/614,748A
;  CURRENT FILING DATE:  2000-07-12
;  PRIOR APPLICATION NUMBER: PCT/US99/00663
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/071,199
;  PRIOR FILING DATE: 1998-01-12
;  PRIOR APPLICATION NUMBER: 60/098,279
;  PRIOR FILING DATE: 1998-08-28
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 1975
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-614-748A-9

Alignment Scores:
Pred. No.:               6.96e-137      Length:        1975
Score:                   1250.50        Matches:       250
Percent Similarity:      64.95%         Conservative:  91
Best Local Similarity:   47.62%         Mismatches:    161
Query Match:             43.28%         Indels:        23
DB:                      4              Gaps:          8

US-10-044-205A-2 (1-553) x US-09-614-748A-9 (1-1975)

Qy          7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSer---AspCys 25
              |||:::|||::::::||||||:::      |||:::||||||:::
Db        261 CTCGAGAACATCGTGGCCAACTCGCTGCTGCTGAAAGCGCGTCAAGGAGGATATGGCAAA 320

Qy         26 AspSerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
                 |||         ::::::   :::      |||   ||||||   :::      |||
Db        321 AAAAGTGGTCGTAGTAAAAAATGGAAGGAGATACTGACACTGCCTCCTGTCAGCCAGTGC 380

Qy         46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
              :::|||||||||      :::      ::::::   |||||||||::::::|||||||||
Db        381 AGTGAGCTTAGACATTCCATTGAAAAGGATTATAGCAGTCTTTGTGACAAGCAACCGATA 440

Qy         66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
              ||||||||||||||||||   |||      |||   ||||||   ::::::
Db        441 GGAAGACGTCTCTTCAGGCAGTTCTGTGATACCAAACCCACTCTAAAGAGGCACATTGAA 500

Qy         86 PheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyProThrLysAsp------ 103
              ||||||:::   |||      :::|||:::|||::::::         |||
Db        501 TTCTTGGATGCAGTGGCAGAATATGAAGTTGCCGATGATGAGGACCGAAGTGATTGTGGA 560

Qy        104 ---SerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGlyAsnPro 122
                 |||   |||                        :::||||||   |||      |||
Db        561 CTGTCAATCTTAGATAGATTCTTCAATGATAAGTTGGCAGCCCCTTTACCAGAAATACCT 620

Qy        123 GlnProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGluGluGlu 142
                                   |||   |||:::|||:::         ||||||
Db        621 CCAGAT---------------GTTGTGACAGAATGTAGATTGGGACTGAAGGAGGAGAAC 665

Qy        143 ArgValAlaAlaValThrLeuArgLysAla------------------GluAlaMetAla 156
                                   :::||||||                     |||
Db        666 ---------------CCTTCCAAAAAAGCCTTTGAGGAATGTACTAGAGTTGCCCATAAC 710

Qy        157 PheLeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeu 176
              :::|||:::   :::||||||:::::::::      |||:::::::::   :::||||||
Db        711 TACCTAAGAGGGGAACCATTTGAAGAATACCAAGAAAGCTCATATTTTTCTCAGTTTTTA 770
```

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Qy      177 GlnTrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgVal 196
            |||||||||      |||   |||||||||:::         |||      :::||||||
Db      771 CAATGGAAATGGCTGGAAAGGCAACCCGTAACAAAGAACACATTTAGACATTACAGAGTT 830

Qy      197 LeuGlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMet 216
            |||||||||||||||||||||||||||||||||   ||||||:::   ||||||||||||
Db      831 CTAGGAAAAGGCGGATTTGGAGAGGTTTGCGCCTGTCAAGTGCGAGCCACAGGAAAAATG 890

Qy      217 TyrAlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAla 236
            ||||||||||||||||||   |||||||||:::||||||:::   ||||||   ||||||
Db      891 TATGCCTGCAAAAAGCTACAAAAAAAAAGAATAAAGAAGAGGAAAGGTGAAGCTATGGCT 950

Qy      237 LeuLeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyr 256
            |||   ||||||   |||||||||||||||   |||   |||:::|||||||||||||||
Db      951 CTAAATGAGAAAAGAATTCTGGAGAAAGTGCAAAGTAGATTCGTAGTTAGTTTAGCCTAC 1010

Qy      257 AlaPheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeu 276
            |||:::|||:::|||      ||||||||||||:::::::::||||||||||||||||||
Db     1011 GCTTATGAAACCAAAGATGCCTTGTGCTTGGTGCTCACCATTATGAATGGAGGGGATTTG 1070

Qy      277 LysPheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyr 296
            ||||||||||||||||||:::|||      |||   |||      |||   :::||||||
Db     1071 AAGTTTCACATTTACAACCTGGGCAATCCCGGCTTTGATGAGCAGAGAGCCGTTTTCTAT 1130

Qy      297 SerAlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAsp 316
            :::|||::::::   ||||||:::      |||            |||||||||||||||
Db     1131 GCTGCAGAGCTGTGTTGCGGCTTGGAAGATTTACAGAGGGAAAGAATTGTATACAGAGAC 1190

Qy      317 MetLysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGly 336
            :::||||||||||||:::||||||||||||   |||:::   |||:::||||||||||||
Db     1191 TTGAAGCCTGAGAATATTCTCCTTGATGATCGTGGACACATCCGGATTTCAGACCTCGGT 1250

Qy      337 LeuAlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyr 356
            ||||||   |||:::      |||:::   :::      |||   ||||||   ||||||
Db     1251 TTGGCCACAGAGATCCCAGAAGGACAGAGGGTTCGAGGAAGAGTTGGAACAGTCGGCTAC 1310

Qy      357 MetAlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAla 376
            ||||||||||||::::::      :::      |||::::::      ||||||:::   
Db     1311 ATGGCACCTGAAGTTGTCAATAATGAA---AAGTATACGTTTAGTCCCGATTGGTGGGGA 1367

Qy      377 MetGlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGlu 396
            :::||||||   ||||||||||||:::   |||   :::|||||||||   |||||||||
Db     1368 CTTGGCTGTCTGATCTATGAAATGATTCAGGGACATTCTCCATTCAAAAAATACAAAGAG 1427

Qy      397 LysValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHis 416
            ||||||      |||::::::   ||||||         |||      ::::::      
Db     1428 AAAGTCAAATGGGAGGAGGTCGATCAAAGAATCAAGAATGATACCGAGGAGTATTCT--- 1484

Qy      417 AspAsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGlu 436
            :::   |||:::|||:::||||||   |||||||||:::   |||   |||   |||   
Db     1485 GAGAAGTTTTCAGAGGATGCCAAATCTATCTGCAGGATGTTACTCACCAAGAATCCAAGC 1544

Qy      437 GlnArgLeuGlySerArg---GluLysSerAspAspProArgLysHisHisPhePheLys 455
            :::|||||||||   |||   |||   :::         ::::::|||      ||||||
Db     1545 AAGCGGCTGGGCTGCAGGGGCGAGGGAGCGGCTGGGGTGAAGCAGCACCCCGTGTTCAAG 1604

Qy      456 ThrIleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAspPro 475
               |||||||||   ||||||||||||   ::::::||||||||||||   |||||||||
Db     1605 GACATCAACTTCAGGAGGCTGGAGGCAAACATGCTGGAGCCCCCTTTCTGTCCTGATCCT 1664

Qy      476 SerValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGlyVal 495
                  ||||||   ||||||:::   :::|||:::   ||||||   |||:::|||:::
Db     1665 CATGCCGTTTACTGTAAGGACGTCCTGGATATCGAGCAGTTCTCGGCGGTGAAAGGATC 1724

Qy      496 GluPheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIle 515
                  |||      |||:::   |||:::      ||||||||||||   |||   |||
Db     1725 TACCTGGACACCGCAGATGAAGACTTCTATGCTCGGTTTGCTACCGGGTGTGTCTCCATC 1784

Qy      516 AlaTrpGlnGluGlu 520
               ||||||   |||
Db     1785 CCCTGGCAGAATGAG 1799
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```
RESULT 13
US-09-614-748A-8
; Sequence 8, Application US/09614748A
; Patent No. 6660474
; GENERAL INFORMATION:
;  APPLICANT: FELDER, ROBIN A.
;  APPLICANT:  JOSE, PEDRO
;  TITLE OF INVENTION: G PROTEIN-RELATED KINASE MUTANTS IN ESSENTIAL
;  TITLE OF INVENTION:  HYPERTENSION
;  FILE REFERENCE: FELDER 3.9-001 CONT
;  CURRENT APPLICATION NUMBER: US/09/614,748A
;  CURRENT FILING DATE:  2000-07-12
;  PRIOR APPLICATION NUMBER: PCT/US99/00663
;  PRIOR FILING DATE: 1999-01-12
;  PRIOR APPLICATION NUMBER: 60/071,199
;  PRIOR FILING DATE: 1998-01-12
;  PRIOR APPLICATION NUMBER: 60/098,279
;  PRIOR FILING DATE: 1998-08-28
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 2017
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-614-748A-8

Alignment Scores:
Pred. No.:              4.81e-136      Length:        2017
Score:                  1243.50        Matches:       248
Percent Similarity:     62.99%         Conservative:  89
Best Local Similarity:  46.36%         Mismatches:    145
Query Match:            43.04%         Indels:        53
DB:                     4              Gaps:          8

US-10-044-205A-2 (1-553) x US-09-614-748A-8 (1-2017)

Qy        7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSerAspCysAsp 26
            |||:::|||::::::||||||:::      |||:::||||||:::      |||      
Db      261 CTCGAGAACATCGTGGCCAACTCGCTGCTGCTGAAAGCGCGTCAAGAAAAGGAT------ 314

Qy       27 SerLysGluLeuGlnArgArgArgArgSerLeuAlaLeuProGlyLeuGlnGlyCysAla 46

Db      314 ------------------------------------------------------------ 314

Qy       47 GluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIleGly 66
                                       :::   |||||||||::::::||||||||||||
Db      315 ---------------------------TATAGCAGTCTTTGTGACAAGCAACCGATAGGA 347

Qy       67 ArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThrPhe 86
            |||||||||||||||   |||      |||   ||||||   ::::::         |||
Db      348 AGACGTCTCTTCAGGCAGTTCTGTGATACCAAACCCACTCTAAAGAGGCACATTGAATTC 407

Qy       87 LeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyProThrLysAsp--------- 103
            |||:::   |||      :::|||:::|||::::::            |||         
Db      408 TTGGATGCAGTGGCAGAATATGAAGTTGCCGATGATGAGGACCGAAGTGATTGTGGACTG 467

Qy      104 SerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGlyAsnProGln 123
            |||   |||                        :::||||||   |||      |||   
Db      468 TCAATCTTAGATAGATTCTTCAATGATAAGTTGGCAGCCCCTTTACCAGAAATACCTCCA 527

Qy      124 ProPheLeuSerGlnAlaValAlaThrLysCysGlnAlaAlaThrThrGluGluGluArg 143
                              |||   |||:::|||:::            ||||||      
Db      528 GAT---------------GTTGTGACAGAATGTAGATTGGGACTGAAGGAGGAGAAC--- 569

Qy      144 ValAlaAlaValThrLeuArgLysAla------------------GluAlaMetAlaPhe 157
                              :::||||||                     |||      :::
Db      570 ------------CCTTCCAAAAAAGCCTTTGAGGAATGTACTAGAGTTGCCCATAACTAC 617

Qy      158 LeuGlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGln 177
            |||:::   :::||||||:::::::::      |||:::::::::   :::|||||||||
Db      618 CTAAGAGGGGAACCATTTGAAGAATACCAAGAAAGCTCATATTTTTCTCAGTTTTTACAA 677

Qy      178 TrpLysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeu 197
```

```
             ||||||      |||   |||||||||:::         |||      :::|||||||||
Db       678 TGGAAATGGCTGGAAAGGCAACCCGTAACAAAGAACACATTTAGACATTACAGAGTTCTA 737

Qy       198 GlyLysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyr 217
             ||||||||||||||||||||||||||||||   ||||||:::   |||||||||||||||
Db       738 GGAAAAGGCGGATTTGGAGAGGTTTGCGCCTGTCAAGTGCGAGCCACAGGAAAAATGTAT 797

Qy       218 AlaCysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeu 237
             |||||||||||||||   |||||||||:::||||||:::   ||||||   |||||||||
Db       798 GCCTGCAAAAAGCTACAAAAAAAAAGAATAAAGAAGAGGAAAGGTGAAGCTATGGCTCTA 857

Qy       238 LeuGluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAla 257
                ||||||   |||||||||||||||   |||   |||:::||||||||||||||||||
Db       858 AATGAGAAAAGAATTCTGGAGAAAGTGCAAAGTAGATTCGTAGTTAGTTTAGCCTACGCT 917

Qy       258 PheGluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLys 277
             :::|||:::|||      ||||||||||||:::::::::|||||||||||||||||||||
Db       918 TATGAAACCAAAGATGCCTTGTGCTTGGTGCTCACCATTATGAATGGAGGGGATTTGAAG 977

Qy       278 PheHisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSer 297
             |||||||||||||||:::|||      |||   |||      |||   :::||||||:::
Db       978 TTTCACATTTACAACCTGGGCAATCCCGGCTTTGATGAGCAGAGAGCCGTTTTCTATGCT 1037

Qy       298 AlaGlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMet 317
             |||::::::   ||||||:::      |||            |||||||||||||||:::
Db      1038 GCAGAGCTGTGTTGCGGCTTGGAAGATTTACAGAGGGAAAGAATTGTATACAGAGACTTG 1097

Qy       318 LysProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeu 337
             ||||||||||||:::||||||||||||   |||:::   |||:::|||||||||||||||
Db      1098 AAGCCTGAGAATATTCTCCTTGATGATCGTGGACACATCCGGATTTCAGACCTCGGTTTG 1157

Qy       338 AlaValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMet 357
             |||   |||:::      |||:::   :::      |||   ||||||   |||||||||
Db      1158 GCCACAGAGATCCCAGAAGGACAGAGGGTTCGAGGAAGAGTTGGAACAGTCGGCTACATG 1217

Qy       358 AlaProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMet 377
             |||||||||::::::      :::      |||::::::      ||||||:::   :::
Db      1218 GCACCTGAAGTTGTCAATAATGAA---AAGTATACGTTTAGTCCCGATTGGTGGGGACTT 1274

Qy       378 GlyCysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLys 397
             ||||||   ||||||||||||:::   |||   :::|||||||||   ||||||||||||
Db      1275 GGCTGTCTGATCTATGAAATGATTCAGGGACATTCTCCATTCAAAAAATACAAAGAGAAA 1334

Qy       398 ValSerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAsp 417
             |||      |||::::::   ||||||         |||      ::::::      :::
Db      1335 GTCAAATGGGAGGAGGTCGATCAAAGAATCAAGAATGATACCGAGGAGTATTCT---GAG 1391

Qy       418 AsnPheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGln 437
                |||:::|||:::||||||   |||||||||:::   |||   |||   |||   :::
Db      1392 AAGTTTTCAGAGGATGCCAAATCTATCTGCAGGATGTTACTCACCAAGAATCCAAGCAAG 1451

Qy       438 ArgLeuGlySerArg---GluLysSerAspAspProArgLysHisHisPhePheLysThr 456
             |||||||||   |||   |||   :::         ::::::|||      ||||||
Db      1452 CGGCTGGGCTGCAGGGGCGAGGGAGCGGCTGGGGTGAAGCAGCACCCCGTGTTCAAGGAC 1511

Qy       457 IleAsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSer 476
             |||||||||   ||||||||||||   ::::::||||||||||||   |||||||||
Db      1512 ATCAACTTCAGGAGGCTGGAGGCAAACATGCTGGAGCCCCCTTTCTGTCCTGATCCTCAT 1571

Qy       477 ValValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGlu 496
                ||||||   ||||||:::   :::|||:::   ||||||   |||:::|||:::
Db      1572 GCCGTTTACTGTAAGGACGTCCTGGATATCGAGCAGTTCTCGGCGGTGAAAGGGATCTAC 1631

Qy       497 PheAspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAla 516
                |||      |||:::   |||:::      ||||||||||||   |||   |||
Db      1632 CTGGACACCGCAGATGAAGACTTCTATGCTCGGTTTGCTACCGGGTGTGTCTCCATCCCC 1691

Qy       517 TrpGlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
             ||||||   |||:::||||||:::|||   |||:::::::::|||
Db      1692 TGGCAGAATGAGATGATCGAATCCGGGTGTTTCAAAGACATCAAC 1736

RESULT 14
US-08-464-954A-2
```

```
; Sequence 2, Application US/08464954A
; Patent No. 6255069
;  GENERAL INFORMATION:
;    APPLICANT:  BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI,
;    APPLICANT:  PRIYA
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR
;    TITLE OF INVENTION:  MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR
;    TITLE OF INVENTION:  KINASES GRK5 AND GRK6
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jane Massey Licata, Esq.
;      STREET:  Woodland Falls Corporate Park
;      STREET:  210 Lake Drive East, Suite 201
;      CITY:  Cherry Hill
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,954A
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076,084
;      FILING DATE:  June 11, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane Massey Licata
;      REGISTRATION NUMBER:  32,257
;      REFERENCE/DOCKET NUMBER:  JEFF-0118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (609) 779-2400
;      TELEFAX:  (609) 779-8488
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2848
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    ANTI-SENSE:  NO
US-08-464-954A-2

Alignment Scores:
Pred. No.:               2.19e-135      Length:         2848
Score:                   1240.00        Matches:        242
Percent Similarity:      65.36%         Conservative:   107
Best Local Similarity:   45.32%         Mismatches:     165
Query Match:             42.92%         Indels:         20
DB:                      3              Gaps:           7

US-10-044-205A-2 (1-553) x US-08-464-954A-2 (1-2848)

Qy         7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSerAspCysAsp 26
             |||:::|||::::::|||||||||      |||:::||||||:::            :::
Db        69 CTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGGAAAT 128

Qy        27 SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
                |||         ::::::   |||:::   |||      |||   :::      |||
Db       129 CGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCAGTGC 188

Qy        46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
                |||||||||      |||      ::::::|||||||||||||||:::      |||
Db       189 GAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACGCCATT 248

Qy        66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
             ||||||   |||||||||:::|||   ||||||   |||         :::
Db       249 GGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGTCGCC 308

Qy        86 PheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyProThrLys--------- 102
             ||||||:::   |||      :::|||:::      :::         |||
Db          309 TTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATGTGGG 368

Qy          103 AspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGlyAsnPro 122
                            |||      ::::::                     |||      |||
Db          369 CGGCACGTAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGAGGTCCCC 428

Qy          123 GlnProPheLeuSerGlnAlaValAlaThr------------LysCysGlnAlaAlaThr 138
                :::      ::::::                              |||:::
Db          429 CGGCAGCTGGTGACGAACTGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAGACCTTTTC 488

Qy          139 ThrGluGluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeu 158
                   |||      |||:::                                    :::|||
Db          489 CAGGAACTCACCCGGCTG---------------------------ACCCACGAGTACCTG 521

Qy          159 GlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrp 178
                         ||||||   |||::::::   |||   ::::::::::::||||||||||||
Db          522 AGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGG 581

Qy          179 LysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGly 198
                |||      |||   |||||||||:::         |||   ::::::||||||||||||
Db          582 AAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGC 641

Qy          199 LysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAla 218
                |||||||||||||||||||||||||||   ||||||:::   ||||||||||||||||||
Db          642 AAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCC 701

Qy          219 CysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeu 238
                ||||||||||||:::|||||||||:::||||||:::   ||||||   |||||||||
Db          702 TGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAAC 761

Qy          239 GluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPhe 258
                ||||||:::|||||||||||||||:::|||   |||:::||||||||||||||||||:::
Db          762 GAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTAT 821

Qy          259 GluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPhe 278
                |||:::|||      ||||||||||||::::::|||||||||||||||||||||||||||
Db          822 GAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTC 881

Qy          279 HisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAla 298
                |||||||||::::::|||      |||         :::|||   :::||||||:::|||
Db          882 CACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCC 941

Qy          299 GlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLys 318
                :::|||   ||||||:::      ||||||         |||||||||||||||:::|||
Db          942 GAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAG 1001

Qy          319 ProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAla 338
                |||||||||:::||||||||||||   |||:::   |||:::||||||||||||||||||
Db         1002 CCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCT 1061

Qy          339 ValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAla 358
                |||   :::      |||:::   |||      |||   ||||||   ||||||||||||
Db         1062 GTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCT 1121

Qy          359 ProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGly 378
                ||||||::::::      :::      |||::::::      ||||||:::|||:::|||
Db         1122 CCGGAGGTGGTGAAGAATGAA---CGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGC 1178

Qy          379 CysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysVal 398
                |||   :::|||||||||:::   |||::::::||||||:::      |||:::|||:::
Db         1179 TGCCTCCTGTACGAGATGATCACAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATC 1238

Qy          399 SerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsn 418
                   :::|||::::::   :::|||   :::::::::      :::         :::
Db         1239 AAGCGGGAGGAGGTG---GAGCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGG 1295

Qy          419 PheThrGluGluAlaLysAspIleCysArgLeuPheLeuAlaLysLysProGluGlnArg 438
                |||:::   :::|||:::   :::|||         |||   |||   |||   :::|||
Db         1296 TTTTCCCCGCAGGCCCGCTCACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGC 1355

Qy          439 LeuGlySerArgGluLysSer---AspAspProArgLysHisHisPhePheLysThrIle 457
                ||||||   |||      |||      :::   ::::::|||      ||||||   :::
Db         1356 CTGGGGTGTCGTGGGGGCAGTGCCCGCGAGGTGAAGGAGCACCCCTCTTTAAGAAGCTG 1415

Qy          458 AsnPheProArgLeuGluAlaGlyLeuIleGluProProPheValProAspProSerVal 477
                ||||||   ||||||   ||||||::::::||||||||||||   |||||||||
Db         1416 AACTTCAAGCGGCTGGGAGCTGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCC 1475

Qy          478 ValTyrAlaLysAspIleAlaGluIleAspAspPheSerGluValArgGlyValGluPhe 497
                :::|||   ||||||:::   :::|||:::   ||||||   |||:::||||||||||||
Db         1476 ATTTACTGCAAGGATGTTCTGGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTG 1535

Qy          498 AspAspLysAspLysGlnPhePheLysAsnPheAlaThrGlyAlaValProIleAlaTrp 517
                :::      |||:::||||||::::::   ||||||||||||:::|||||||||   |||
Db         1536 GAGCCTACCGACCAGCAGTTCTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGG 1595

Qy          518 GlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
                |||   |||::::::||||||      |||:::|||||||||
Db         1596 CAGAACGAGATGGTGGAGACCGAGTGCTTCCAAGAGCTGAAT 1637
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RESULT 15
US-08-221-817-12
; Sequence 12, Application US/08221817
; Patent No. 5532151
; GENERAL INFORMATION:
; APPLICANT: Chantry, David
; APPLICANT: Gray, Patrick W.
; APPLICANT: Hoekstra, Merle F.
; TITLE OF INVENTION: A No. 5532151el G Protein-Coupled Receptor
; TITLE OF INVENTION: Kinase GRK6
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,817
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/123,932
; FILING DATE: 17 SEP 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532151and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31981
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2204 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 31..1758
US-08-221-817-12

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Alignment Scores:
Pred. No.:              2.47e-135     Length:          2204
Score:                  1238.00       Matches:         242
Percent Similarity:     65.36%        Conservative:    107
Best Local Similarity:  45.32%        Mismatches:      165
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Query Match:          42.85%    Indels:    20
DB:                   1         Gaps:       7

US-10-044-205A-2 (1-553) x US-08-221-817-12 (1-2204)

Qy        7 LeuAspAsnLeuIleAlaAsnThrAlaTyrLeuGlnAlaArgLysProSerAspCysAsp 26
            |||:::|||::::::|||||||||      |||:::||||||:::            :::
Db       37 CTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGGAAAT 96

Qy       27 SerLysGluLeuGlnArgArg---ArgArgSerLeuAlaLeuProGlyLeuGlnGlyCys 45
               |||         ::::::   |||:::   |||      |||   :::      |||
Db       97 CGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCAGTGC 156

Qy       46 AlaGluLeuArgGlnLysLeuSerLeuAsnPheHisSerLeuCysGluGlnGlnProIle 65
               |||||||||      |||      ::::::|||||||||||||||:::      |||
Db      157 GAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACCGCATT 216

Qy       66 GlyArgArgLeuPheArgAspPheLeuAlaThrValProThrPheArgLysAlaAlaThr 85
            ||||||   |||||||||:::|||   ||||||   |||         :::
Db      217 GGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGTCGCC 276

Qy       86 PheLeuGluAspValGlnAsnTrpGluLeuAlaGluGluGlyProThrLys--------- 102
            ||||||:::   |||      :::|||:::      :::         |||
Db      277 TTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATGTGGG 336

Qy      103 AspSerAlaLeuGlnGlyLeuValAlaThrCysAlaSerAlaProAlaProGlyAsnPro 122
                        |||      ::::::                     |||      |||
Db      337 CGGCACGTAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGAGGTCCCC 396

Qy      123 GlnProPheLeuSerGlnAlaValAlaThr------------LysCysGlnAlaAlaThr 138
            :::      ::::::                              |||:::
Db      397 CGGCAGCTGGTGACGAACTGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAGACCTTTTC 456

Qy      139 ThrGluGluGluArgValAlaAlaValThrLeuArgLysAlaGluAlaMetAlaPheLeu 158
               |||      |||:::                                    :::|||
Db      457 CAGGAACTCACCCGGCTG--------------------------ACCCACGAGTACCTG 489

Qy      159 GlnGluGlnProPheLysAspPheValThrSerAlaPheTyrAspLysPheLeuGlnTrp 178
                     ||||||   |||::::::   |||   ::::::::::::||||||||||||
Db      490 AGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGG 549

Qy      179 LysLeuPheGluMetGlnProValSerAspLysTyrPheThrGluPheArgValLeuGly 198
            |||      |||   |||||||||:::         |||   ::::::||||||||||||
Db      550 AAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGT 609

Qy      199 LysGlyGlyPheGlyGluValCysAlaValGlnValLysAsnThrGlyLysMetTyrAla 218
            |||||||||||||||||||||||||||   ||||||:::   ||||||||||||||||||
Db      610 AAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCC 669

Qy      219 CysLysLysLeuAspLysLysArgLeuLysLysLysGlyGlyGluLysMetAlaLeuLeu 238
            ||||||||||||:::|||||||||:::||||||:::   ||||||   |||||||||
Db      670 TGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAAC 729

Qy      239 GluLysGluIleLeuGluLysValSerSerProPheIleValSerLeuAlaTyrAlaPhe 258
            ||||||:::|||||||||||||||:::|||   |||:::||||||||||||||||||:::
Db      730 GAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTAT 789

Qy      259 GluSerLysThrHisLeuCysLeuValMetSerLeuMetAsnGlyGlyAspLeuLysPhe 278
            |||:::|||      ||||||||||||::::::|||||||||||||||||||||||||||
Db      790 GAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTC 849

Qy      279 HisIleTyrAsnValGlyThrArgGlyLeuAspMetSerArgValIlePheTyrSerAla 298
            |||||||||::::::|||      |||         :::|||   :::||||||:::|||
Db      850 CACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCC 909

Qy      299 GlnIleAlaCysGlyMetLeuHisLeuHisGluLeuGlyIleValTyrArgAspMetLys 318
            :::|||   ||||||:::      ||||||         |||||||||||||||:::|||
Db      910 GAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAG 969

Qy      319 ProGluAsnValLeuLeuAspAspLeuGlyAsnCysArgLeuSerAspLeuGlyLeuAla 338
            |||||||||:::||||||||||||   |||:::   |||:::||||||||||||||||||
Db      970 CCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCT 1029

Qy      339 ValGluMetLysGlyGlyLysProIleThrGlnArgAlaGlyThrAsnGlyTyrMetAla 358
            |||   :::      |||:::   |||      |||   ||||||   ||||||||||||
Db     1030 GTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCT 1089

Qy      359 ProGluIleLeuMetGluLysValSerTyrSerTyrProValAspTrpPheAlaMetGly 378
            ||||||::::::      :::      |||::::::      ||||||:::|||:::|||
Db     1090 CCGGAGGTGGTGAAGAATGAA---CGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGC 1146

Qy      379 CysSerIleTyrGluMetValAlaGlyArgThrProPheLysAspTyrLysGluLysVal 398
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Db     1147 TGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATC 1206

Qy      399 SerLysGluAspLeuLysGlnArgThrLeuGlnAspGluValLysPheGlnHisAspAsn 418
               :::|||::::::   :::|||   :::::::::      :::         :::
Db     1207 AAGCGGGAGGAGGTG---GAGCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGC 1263

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Qy      518 GlnGluGluIleIleGluThrGlyLeuPheGluGluLeuAsn 531
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Job time : 149 secs
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              Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:        August 13, 2004, 14:01:20 ; Search time 692.966 Seconds
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Perfect score: 2198
Sequence:      1 gaccctaagatgaagggacc..........aacactcaggtttatttga 2198

Scoring table: IDENTITY_NUC
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Searched:      3225727 seqs, 2453303834 residues

Total number of hits satisfying chosen parameters:      6451454

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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      Pred. No. is the number of results predicted by chance to have a
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  No.    Score   Match Length DB  ID                          Description
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    2   2008.8    91.4   2249 15  US-10-217-745-5              Sequence 5, Appli
    3     1659    75.5   1659 14  US-10-044-205A-3             Sequence 3, Appli
    4   1658.8    75.5   1662 17  US-10-311-034-45             Sequence 45, Appl
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                              ALIGNMENTS


RESULT 1
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; Sequence 1, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
;  APPLICANT: KAPELLER-LIBERMANN, Rosana
;  APPLICANT:  BANDARU, Rajasekhar
;  TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protei
;  TITLE OF INVENTION:  Uses Thereof
;  FILE REFERENCE: 10147-52U1
;  CURRENT APPLICATION NUMBER: US/10/044,205A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: US 60/242,428
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: US 60/241,884
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 60/241,877
;  PRIOR FILING DATE: 2000-10-20
;  NUMBER OF SEQ ID NOS: 44
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; SEQ ID NO 1
;   LENGTH: 2198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-044-205A-1

  Query Match             100.0%;  Score 2198;  DB 14;  Length 2198;
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; Sequence 5, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases ar
;  TITLE OF INVENTION:  Polynucleotides
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/10/217,745
;  CURRENT FILING DATE:  2002-08-12
;  PRIOR APPLICATION NUMBER: US/09/802,117
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 2249
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-217-745-5

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGC 417

Qy        355 CCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGC 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 CCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGC 477

Qy        415 TGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGC 474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 TGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGC 537

Qy        475 AGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCA 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCA 597

Qy        535 AGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCA 594
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 AGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCA 657

Qy        595 AAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACC 654
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 AAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACC 717

Qy        655 CGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAG 714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 CGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAG 777

Qy        715 AGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGC 774
              |||||||||||||||||||||||  |||||||||||||||||||||||||||||||||||
Db        778 AGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGC 837

Qy        775 CCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCG 834
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 CCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCG 897

Qy        835 AGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTT 894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 AGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTT 957

Qy        895 TTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAAC 954
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 TTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAAC 1017

Qy        955 TGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAA 1014
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 TGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAA 1077

Qy       1015 TCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGA 1074
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 TCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGA 1137

Qy       1075 CCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACA 1134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 CCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACA 1197

Qy       1135 ACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCT 1194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 ACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCT 1257

Qy       1195 GTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATG 1254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1258 GTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATG 1317

Qy       1255 TGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGA 1314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1318 TGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGA 1377

Qy       1315 AGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCC 1374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1378 AGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCC 1437

Qy       1375 TAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTT 1434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1438 TAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTT 1497

Qy       1435 ATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGG 1494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1498 ATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGG 1557

Qy       1495 ATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGG 1554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1558 ATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGG 1617

Qy       1555 AAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCA 1614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1618 AAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCA 1677

Qy       1615 GAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCC 1674
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1678 GAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCC 1737

Qy       1675 TGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAG 1734
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1738 TGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAG 1797

Qy       1735 ACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATA 1794
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1798 ACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATA 1857

Qy       1795 AGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTA 1854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1858 AGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTA 1917

Qy       1855 TAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGG 1914
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1918 TAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGG 1977

Qy       1915 GTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGG 1974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1978 GTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGG 2037

Qy       1975 CAGCAGGAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAATG 2034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2038 CAGCAGGAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAATG 2097

Qy       2035 AGGGCTAATCAGTTAGGAGGGACATCACAACCACAAAACAATTCAAAAGACAGGCAAGCT 2094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2098 AGGGCTAATCAGTTAGGAGGGACATCACAACCACAAAACAATTCAAAAGACAGGCAAGCT 2157

Qy       2095 CACTACTAGAACACATTTTATTTTCTTTTTCTTTCTTCATAAAGATGAGTAAAGTCTCAG 2154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2158 CACTACTAGAACACATTTTATTTTCTTTTTCTTTCTTCATAAAGATGAGTAAAGTCTCAG 2217

Qy       2155 TTTTCACTGAGGGCAGGGAAAAGGAACACTCA 2186
              ||||||||||||||||||||||||||||||||
Db       2218 TTTTCACTGAGGGCAGGGAAAAGGAACACTCA 2249


RESULT 3
US-10-044-205A-3
; Sequence 3, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
;  APPLICANT: KAPELLER-LIBERMANN, Rosana
;  APPLICANT:  BANDARU, Rajasekhar
;  TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protei
;  TITLE OF INVENTION:  Uses Thereof
;  FILE REFERENCE: 10147-52U1
;  CURRENT APPLICATION NUMBER: US/10/044,205A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: US 60/242,428
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: US 60/241,884
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 60/241,877
;  PRIOR FILING DATE: 2000-10-20
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
;   LENGTH: 1659
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-044-205A-3

  Query Match             75.5%;  Score 1659;  DB 14;  Length 1659;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1659;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1949
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 4
US-10-311-034-45
; Sequence 45, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  YUE, Henry
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  BANDMAN, Olga
;  APPLICANT:  BOROWSKY, Mark L.
;  APPLICANT:  AU-YOUNG, Janice
;  APPLICANT:  LU, Yan
;  APPLICANT:  GANDHI, Ameena R.
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  GREENWALD, Sara R.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  KEARNEY, Liam
;  APPLICANT:  BURFORD, Neil
;  APPLICANT:  NGUYEN, Danniel B.
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  HE, Ann
;  APPLICANT:  THORNTON, Michael
;  APPLICANT:  HAFALIA, April
;  APPLICANT:  ARVIZU, Chandra S.
;  APPLICANT:  GURURAJAN, Rajagopal
;  APPLICANT:  LO, Terence P.
;  APPLICANT:  KHAH, Farrah A.
;  APPLICANT:  RECIPON, Shirley A.
;  APPLICANT:  AZIMZAI, Yalda
;  APPLICANT:  POLICKY, Jennifer L.
;  APPLICANT:  DING, Li
;  APPLICANT:  GRETHER, Megan
;  APPLICANT:  ELLIOTT, Vicki S.
;  APPLICANT:  THANGAVELU, Kavitha
;  APPLICANT:  BATRA, Sajeev
;  APPLICANT:  ISON, Craig H.
;  TITLE OF INVENTION: HUMAN KINASES
;  FILE REFERENCE: PI-0125 PCT
;  CURRENT APPLICATION NUMBER: US/10/311,034
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
;    60/228,056
;  PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
;    25
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PERL Program
; SEQ ID NO 45
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
US-10-311-034-45

  Query Match             75.5%;  Score 1658.8;  DB 17;  Length 1662;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1660;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
              ||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662


RESULT 5
US-10-451-168-49
; Sequence 49, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
;  APPLICANT: SMITHKLINE BEECHAM CORPORATION
;  APPLICANT:  SMITHKLINE BEECHAM p.l.c.
;  APPLICANT:  GLAXO GROUP LIMITED
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GP50039
;  CURRENT APPLICATION NUMBER: US/10/451,168
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: PCT/US01/49232
;  PRIOR FILING DATE: 2000-12-17
;  PRIOR APPLICATION NUMBER: 60/256,710
;  PRIOR FILING DATE: 2000-12-19
;  PRIOR APPLICATION NUMBER: 60/257,048
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: 60/260,482
;  PRIOR FILING DATE: 2001-01-09
;  PRIOR APPLICATION NUMBER: 60/264,922
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/266,797
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/276,988
;  PRIOR FILING DATE: 2001-03-19
;  PRIOR APPLICATION NUMBER: 60/281,535
;  PRIOR FILING DATE: 2001-04-04
;  PRIOR APPLICATION NUMBER: 60/289,622
;  PRIOR FILING DATE: 2002-06-28
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-451-168-49

  Query Match             75.5%;  Score 1658.8;  DB 17;  Length 1662;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1660;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy         1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy         1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy         1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy         1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy         1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy         1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy         1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy         1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy         1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy         1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy         1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
                ||||||||||||||||||||||||||||||||||||||||||
Db         1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662


RESULT 6
US-10-217-745-1
; Sequence 1, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases an
;  TITLE OF INVENTION:  Polynucleotides
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/10/217,745
;  CURRENT FILING DATE:  2002-08-12
;  PRIOR APPLICATION NUMBER: US/09/802,117
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-217-745-1

  Query Match             75.5%;  Score 1658.4;  DB 15;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1659;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
                |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db            1 ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy          351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy          411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy          471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy          531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy          591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy          651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy          711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
                |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db          421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy          771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy          831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy          891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy          951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy         1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy         1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy         1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy         1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy         1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy         1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy         1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy         1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy         1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy         1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy         1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy         1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy         1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy         1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy         1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
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Db         1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662
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RESULT 7
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV
;  CURRENT APPLICATION NUMBER: US/09/964,469
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Human
US-09-964-469-1

  Query Match             75.4%;  Score 1657.2;  DB 9;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1659;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db            1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy          351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy          411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy          471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy          531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy          591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy          651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy          711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
                |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db          421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy          771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy          831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy          891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 950
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660

Qy          951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy         1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy         1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy         1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy         1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy         1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
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Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
              ||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662

RESULT 8
US-10-425-962-1
; Sequence 1, Application US/10425962
; Publication No. US20030180786A1
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV2
;  CURRENT APPLICATION NUMBER: US/10/425,962
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: 09/964,469
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-425-962-1

  Query Match             75.4%;  Score 1657.2;  DB 15;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1659;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
              ||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662


RESULT 9
US-10-072-012-273
; Sequence 273, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
;  APPLICANT: Tchernev, Velizar
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Li, Li
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Taupier Jr, Raymond J.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Wolenc, Adam R.
;  APPLICANT:  Pena, Carol E. A
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Grosse, William M.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-258
;  CURRENT APPLICATION NUMBER: US/10/072,012
;  CURRENT FILING DATE:  2002-01-31
;  PRIOR APPLICATION NUMBER: 60/265,102
;  PRIOR FILING DATE: 2001-01-30
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;  PRIOR APPLICATION NUMBER: 60/265,514
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,517
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,412
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,395
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/266,406
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/266,767
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: 60/267,057
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/266,975
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/267,459
;  PRIOR FILING DATE: 2001-02-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1391
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
;   LENGTH: 1701
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-072-012-273

  Query Match             74.6%;  Score 1640.8;  DB 13;  Length 1701;
  Best Local Similarity   98.7%;  Pred. No. 0;
  Matches 1693;  Conservative    0;  Mismatches    2;  Indels   21;  Gaps    3;

Qy        273 TGCGCCCCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACC 332
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TGCGCCCCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACC 60

Qy        333 GCCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGG 392
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGG 120

Qy        393 CGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTG 452
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTG 180

Qy        453 AACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTA 512
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTA 240

Qy        513 GCCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAG 572
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GCCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAG 300

Qy        573 CTGGCCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCG 632
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGGCCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCG 360

Qy        633 AGTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGC 692
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AGTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGC 420

Qy        693 CAAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCC 752
              |||||||||||||||||||||||||||||||||||||||||||||  |||||||||||||
Db        421 CAAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCC 480

Qy        753 ATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAG 812
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 ATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAG 540

Qy        813 TTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTC 872
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTC 600

Qy        873 AGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGG 932
              |||||||||||||||||||||||||||||||||               ||||||||||||
Db    601 AGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTA---------------AAAAACACTGGG 645

Qy    933 AAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAG 992
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    646 AAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAG 705

Qy    993 ATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTG 1052
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    706 ATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTG 765

Qy   1053 GCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGA 1112
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    766 GCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGA 825

Qy   1113 GACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATC 1172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    826 GACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATC 885

Qy   1173 TTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTAT 1232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    886 TTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTAT 945

Qy   1233 CGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGAC 1292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    946 CGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGAC 1005

Qy   1293 CTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAG---GGCTGGAACC 1349
          |||||||||||||||||||||||||||||||||||||||||||||||   ||||||||||
Db   1006 CTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGCAGGCTGGAACC 1065

Qy   1350 AATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGAC 1409
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1066 AATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGAC 1125

Qy   1410 TGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGAT 1469
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1126 TGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGAT 1185

Qy   1470 TACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAA 1529
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1186 TACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAA 1245

Qy   1530 TTCCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAG 1589
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1246 TTCCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAG 1305

Qy   1590 AAACCAGAGCAACGCTTAGGAAGC---AGAGAAAAGTCTGATGATCCCAGGAAACATCAT 1646
          ||||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db   1306 AAACCAGAGCAACGCTTAGGAAGCAGGAGAGAAAAGTCTGATGATCCCAGGAAACATCAT 1365

Qy   1647 TTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTG 1706
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1366 TTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTG 1425

Qy   1707 CCAGACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTT 1766
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1426 CCAGACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTT 1485

Qy   1767 CGGGGGGTGGAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCT 1826
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1486 CGGGGGGTGGAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCT 1545

Qy   1827 GTTCCTATAGCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGAC 1886
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1546 GTTCCTATAGCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGAC 1605

Qy   1887 CCCAACAGACCTACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTA 1946
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1606 CCCAACAGACCTACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTA 1665

Qy   1947 TTGTAAATTGCTCTCTTTACCAGACAGGCAGCAGGA 1982
          ||||||||||||||||||||||||||||||||||||
Db   1666 TTGTAAATTGCTCTCTTTACCAGACAGGCAGCAGGA 1701
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RESULT 10
US-10-217-745-3
; Sequence 3, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases anc
;  TITLE OF INVENTION:  Polynucleotides
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/10/217,745
;  CURRENT FILING DATE:  2002-08-12
;  PRIOR APPLICATION NUMBER: US/09/802,117
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1062
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-217-745-3

  Query Match             47.6%;  Score 1046.8;  DB 15;  Length 1062;
  Best Local Similarity   99.8%;  Pred. No. 1.7e-308;
  Matches 1048;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy    351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy    411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy    471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy    531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy    591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy    651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy    711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
          |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db    421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy    771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy    831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy    891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
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Qy      951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy     1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy     1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy     1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy     1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy     1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy     1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1340
            ||||||||||||||||||||||||||||||
Db     1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1050


RESULT 11
US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV
;  CURRENT APPLICATION NUMBER: US/09/964,469
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 36651
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(36651)
;   OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

  Query Match             39.5%;  Score 867.4;  DB 9;  Length 36651;
  Best Local Similarity   95.1%;  Pred. No. 1.1e-252;
  Matches  895;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy        1 GACCCTAAGATGAAGGACCTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTGCTTTC 60
            ||||||||||||||||||||         ||      |||| |      |||  ||||||
Db     1786 GACCCTAAGATGAAGGACCAGTGGGGAGGTGGCCCCGGCAGGTGTCCCAGCAGCTTTC 1845

Qy       61 GCCTTGGCAGGTGGAGCATGACCTATCGTGTGCAGTTCCTGGCGGGCTATACATAGCCA 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1846 GCCTTGGCAGGTGGAGCATGACCTATCGTGTGCAGTTCCTGGCGGGCTATACATAGCCA 1905

Qy      121 GTCAAAGCTTCTTACAAAAGAAACCTCTTTCACACCCTCCACGGGTCCCACCCACAGGCC 180
            ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db     1906 GTCAAAGCTTCTTACAAGAGAAACCTCTTTCACACCCTCCACGGGTCCCACCCACAGGCC 1965

Qy      181 ACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCA 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1966 ACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCA 2025

Qy      241 GCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACA 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2026 GCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACA 2085

Qy      301 TGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2086 TGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGG 2145

Qy      361 ACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGG 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2146 ACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGG 2205

Qy      421 GCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGC 480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2206 GCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGC 2265

Qy      481 CCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGG 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2266 CCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGG 2325

Qy      541 CAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACA 600
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2326 CAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACA 2385

Qy      601 GCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAAC 660
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2386 GCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAAC 2445

Qy      661 CCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAG 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2446 CCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAG 2505

Qy      721 TGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTA 780
            |||||||||||||||||  |||||||||||||||||||||||||||||||||||||||||
Db     2506 TGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTA 2565

Qy      781 AGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2566 AGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGC 2625

Qy      841 AACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2626 AACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGG 2685

Qy      901 AGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTAT 941
            ||||| ||| |  ||||  |  |  |     |  || | ||
Db     2686 AGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCAT 2726


RESULT 12
US-10-425-962-3
; Sequence 3, Application US/10425962
; Publication No. US20030180786A1
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV2
;  CURRENT APPLICATION NUMBER: US/10/425,962
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: 09/964,469
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 36651
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(36651)
;   OTHER INFORMATION: n = A,T,C or G
US-10-425-962-3

  Query Match             39.5%;  Score 867.4;  DB 15;  Length 36651;
  Best Local Similarity   95.1%;  Pred. No. 1.1e-252;
  Matches  895;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy           1 GACCCTAAGATGAAGGACCTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTGCTTTC 60
               ||||||||||||||||||||         ||      |||| |      |||  ||||||
Db        1786 GACCCTAAGATGAAGGACCAGTGGGGGAGGTGGCCCCGGCAGGTGTCCCAGCAGCTTTC 1845

Qy          61 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGCAGTTCCTGGCGGGCTATACATAGCCA 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1846 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGCAGTTCCTGGCGGGCTATACATAGCCA 1905

Qy         121 GTCAAAGCTTCTTACAAAAGAAACCTCTTTCACACCCTCCACGGGTCCCACCCACAGGCC 180
               ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        1906 GTCAAAGCTTCTTACAAGAGAAACCTCTTTCACACCCTCCACGGGTCCCACCCACAGGCC 1965

Qy         181 ACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCA 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1966 ACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCA 2025

Qy         241 GCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACA 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2026 GCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACA 2085

Qy         301 TGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGG 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2086 TGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGG 2145

Qy         361 ACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2146 ACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGG 2205

Qy         421 GCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGC 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2206 GCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGC 2265

Qy         481 CCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGG 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2266 CCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGG 2325

Qy         541 CAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACA 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2326 CAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACA 2385

Qy         601 GCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGAACCCGCAAC 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2386 GCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGAACCCGCAAC 2445

Qy         661 CCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAG 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2446 CCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAG 2505

Qy         721 TGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTA 780
               |||||||||||||||||  |||||||||||||||||||||||||||||||||||||||||
Db        2506 TGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTA 2565

Qy         781 AGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2566 AGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGC 2625

Qy         841 AACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGG 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2626 AACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGG 2685

Qy         901 AGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTAT 941
               ||||| ||| |  ||||  |  |  |     |  || | ||
Db        2686 AGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCAT 2726

RESULT 13
US-09-851-686-2
; Sequence 2, Application US/09851686
; Patent No. US20020034767A1
; GENERAL INFORMATION:
;  APPLICANT: Benovic, Jeffrey L.
;  APPLICANT:  Gomez, Jorge
;  APPLICANT:  Kunapuli, Priya
;  TITLE OF INVENTION: Compositions and Methods for Modulating the Activity of G Protein-
;  TITLE OF INVENTION:  Receptor Kinases GRK5 and GRK6
;  FILE REFERENCE: JEFF-0118-DIV
;  CURRENT APPLICATION NUMBER: US/09/851,686
;  CURRENT FILING DATE:  2001-10-01
;  PRIOR APPLICATION NUMBER: US 08/464,954
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/076,084
;  PRIOR FILING DATE: 1993-06-11
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 2848
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-851-686-2

  Query Match             19.0%;  Score 418.2;  DB 9;  Length 2848;
  Best Local Similarity   56.2%;  Pred. No. 4.2e-116;
  Matches  890;  Conservative    0;  Mismatches  683;  Indels   12;  Gaps    5;

Qy         305 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 364
               ||  || || ||| |  | || ||||| |     ||  |||||||| |       |   |
Db          65 GGAGCTCGAGAACATCGTAGCGAACACGGTACTACTCAAGGCCCGGGAAGGTGGCGGTGG 124

Qy         365 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 421
                 |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db         125 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 184

Qy         422 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 481
                ||||  ||||| || |  |  ||    |   |||  ||||||||||| |||| |||  |
Db         185 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACGC 244

Qy         482 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 541
               ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db         245 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 304

Qy         542 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 601
                 ||||||| || |  |||    | |  ||  || ||  ||| |        || |   |
Db         305 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 364

Qy         602 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGAACCCGCAACC 661
                | || ||| |   |   |   | || |  |||   | | |  || |    |   |
Db         365 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 421

Qy         662 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 721
                 ||| | | |||   ||| | | |  |  || ||| ||     | | |     || |
Db         422 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 480

Qy         722 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781
                 ||            | |  ||||||  ||   |  | | ||   | |   || |||
Db         481 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 538

Qy         782 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 841
                || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db         539 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 598

Qy         842 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901
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US-09-873-367C-142
; Sequence 142, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  APPLICANT:  Soppet, Daniel
;  APPLICANT:  Endress, Gregory
;  APPLICANT:  Augustus, Meena
;  APPLICANT:  Ebner, Reinhard
;  APPLICANT:  Carter, Kenneth
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-64
;  CURRENT APPLICATION NUMBER: US/09/873,367C
;  CURRENT FILING DATE:  2003-04-29
;  PRIOR APPLICATION NUMBER: U.S. 60/236,891
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: U.S. 60/236,842
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: U.S. 60/244,867
;  PRIOR FILING DATE: 2000-11-01
;  PRIOR APPLICATION NUMBER: U.S. 60/245,084
;  PRIOR FILING DATE: 2000-11-01
;  NUMBER OF SEQ ID NOS: 1067
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 142
;   LENGTH: 2848
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-873-367C-142

  Query Match             19.0%;  Score 418.2;  DB 10;  Length 2848;
  Best Local Similarity   56.2%;  Pred. No. 4.2e-116;
  Matches  890;  Conservative    0;  Mismatches  683;  Indels   12;  Gaps    5;

Qy          305 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 364
                ||  || || ||| |  | || ||||| |     ||  |||||||| |       |   |
Db           65 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 124

Qy          365 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 421
                  |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db          125 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 184

Qy          422 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 481
                 ||||  ||||| || |  |  ||    |   |||  ||||||||||| |||| |||  |
Db          185 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACGC 244

Qy          482 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 541
                ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db          245 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 304

Qy          542 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 601
                  ||||||| || |  |||    | |  ||  || ||  ||| |        || |   |
Db          305 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 364

Qy          602 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 661
                 | || ||| |   |   |   | || |  |||   | | |  || |    |   |
Db          365 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 421

Qy          662 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 721
                  ||| | | |||   ||| | | |  |  || ||| ||     | | |     ||  |
Db          422 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 480

Qy          722 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781
                  ||            | |  ||||||  ||   |  | | ||   | |   || |||
Db          481 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 538

Qy          782 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 841
                 || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db          539 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 598

Qy          842 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901
                 |||||| |  | ||   |||||   | | | |||| ||||| |||||||| ||||||||
Db          599 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 658

Qy          902 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 961
                ||| || |||  |||||||     ||| |||||||||||||||| ||||| || || ||
Db          659 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 718

Qy          962 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 1021
                 |||||| | ||||||      || |||   ||||| ||    || ||| | ||| ||||
Db          719 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 778

Qy         1022 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 1081
                ||| || | |||    ||  | ||     ||||||| |||| ||||| ||||  |   ||
Db          779 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTATGAGACCAAGGACGCGCT 838

Qy         1082 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 1141
                 ||||| ||  |||  |||||||| ||||| ||||||||||||||||||||| || ||||
Db          839 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 898

Qy         1142 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 1201
                |  |  |||| |   |      ||||   |||| ||| | ||| ||||   ||||||  |
Db          899 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 958

Qy         1202 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 1261
                |  | |||| ||        ||||||| ||  ||||| ||||||| |||||  |  | ||
Db          959 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 1018

Qy         1262 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1321
                |||||||| |||| ||  | |  | ||||||||||| || || ||| |  ||   |  ||
Db         1019 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1078

Qy         1322 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1381
                | || ||||||    | | |  || |||   |||||||||||||| |||    |  || |
Db         1079 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1135

Qy         1382 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1441
                 || | | | ||  | |        |||||||  ||  | || |||  | | || || ||
Db         1136 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1195

Qy         1442 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1501
                | |  | || |   | || ||| |  |    ||| | ||| |||     |||||  || |
Db         1196 GATCACAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1255

Qy         1502 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1561
                ||          | | | |   |   | |      |       | | |  |||
Db         1256 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGGTTTTCCCCGCAGGCCCGCTC 1315

Qy         1562 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1621
                |  |   |    |||| |||      |     | || |  |      |  |  | |  |
Db         1316 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGCCTGGGGTGTCGTGGGGGCAG 1375

Qy         1622 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1681
                  |    ||    | | | || |   ||||||| | | | |||||    || |||| |||
Db         1376 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1435

Qy         1682 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1741
                |||| |  | || || || ||   ||| |||||    |   ||||   ||| ||
Db         1436 TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGGTCT 1495

Qy         1742 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1801
                 || |||||   | ||||||   |||   ||| |||||  | ||    |  ||  |||||||
Db         1496 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGCAGTT 1555

Qy         1802 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1861
                || | | || ||||| |||||   ||| || ||  | |||||| | || ||  | || ||
Db         1556 CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1615

Qy         1862 GGGACTGTTTGAGGAACTGAATGAC 1886
                 |     ||  | || ||||||| |
Db         1616 CGAGTGCTTCCAAGAGCTGAATGTC 1640


RESULT 14
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Db        599 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 658

Qy        902 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 961
Db        659 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 718

Qy        962 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 1021
Db        719 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 778

Qy       1022 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 1081
Db        779 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTATGAGACCAAGGACGCGCT 838

Qy       1082 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 1141
Db        839 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 898

Qy       1142 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 1201
Db        899 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 958

Qy       1202 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 1261
Db        959 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 1018

Qy       1262 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1321
Db       1019 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1078

Qy       1322 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1381
Db       1079 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1135

Qy       1382 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1441
Db       1136 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1195

Qy       1442 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1501
Db       1196 GATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1255

Qy       1502 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1561
Db       1256 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGCTTTTCCCCGCAGGCCCGCTC 1315

Qy       1562 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1621
Db       1316 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGCCTGGGGTGTCGTGGGGGCAG 1375

Qy       1622 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1681
Db       1376 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1435

Qy       1682 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1741
Db       1436 TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGTTCT 1495

Qy       1742 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1801
Db       1496 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGGACTT 1555

Qy       1802 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1861
Db       1556 CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1615

Qy       1862 GGGACTGTTTGAGGAACTGAATGAC 1886
Db       1616 CGAGTGCTTCCAAGAGCTGAATGTC 1640


RESULT 15
US-10-159-856-4
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; Sequence 4, Application US/10159856
; Publication No. US20030228689A1
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRES
;  FILE REFERENCE: RTS-0365
;  CURRENT APPLICATION NUMBER: US/10/159,856
;  CURRENT FILING DATE:  2002-05-31
;  NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 4
;   LENGTH: 2848
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (63)...(1793)
US-10-159-856-4

  Query Match             19.0%;  Score 418.2;  DB 16;  Length 2848;
  Best Local Similarity   56.2%;  Pred. No. 4.2e-116;
  Matches  890;  Conservative    0;  Mismatches  683;  Indels   12;  Gaps    5;

Qy        305 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 364
Db         65 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 124

Qy        365 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 421
Db        125 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 184

Qy        422 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 481
Db        185 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACGC 244

Qy        482 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 541
Db        245 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 304

Qy        542 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 601
Db        305 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 364

Qy        602 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 661
Db        365 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 421

Qy        662 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 721
Db        422 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 480

Qy        722 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781
Db        481 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 538

Qy        782 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 841
Db        539 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 598

Qy        842 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901
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Qy        902 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 961
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Qy        962 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 1021
Db        719 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 778

Qy       1022 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 1081
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Qy       1082 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 1141
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Qy       1142 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 1201
              |  |  |||| |   |      ||||   |||| ||| | ||| ||||   ||||||  |
Db        899 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 958

Qy       1202 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 1261
              |  | |||| ||        ||||||| ||  ||||| ||||||| |||||  |  | ||
Db        959 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 1018

Qy       1262 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1321
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Qy       1322 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1381
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Qy       1382 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1441
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Search completed: August 13, 2004, 19:06:08
Job time : 698.966 secs
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                    GenCore version 5.1.6
           Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          August 13, 2004, 12:57:35 ; Search time 3850.63 Seconds
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Title:           US-10-044-205A-1
Perfect score:   2198
Sequence:        1 gaccctaagatgaagggacc..........aacactcaggtttattttga 2198

Scoring table:   IDENTITY_NUC
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Searched:        27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters:       55026578

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       EST:*
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              29:  gb_gss2:*

   Pred. No. is the number of results predicted by chance to have a
   score greater than or equal to the score of the result being printed,
   and is derived by analysis of the total score distribution.

                               SUMMARIES
                  %
Result          Query
  No.   Score   Match Length DB  ID                   Description
--------------------------------------------------------------------------
    1   398.6   18.1    2978  11  AK051405            AK051405 Mus muscu
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c   3   311.8   14.2    1201  13  BX404586            BX404586 BX404586
    4   311.6   14.2    2329  11  BC027597            BC027597 Homo sapi
c   5     307   14.0     917  13  BX392018            BX392018 BX392018
    6   304.6   13.9    1721  29  AY406080            AY406080 Homo sapi
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    8   299.2   13.6    1019  13  BQ061148            BQ061148 AGENCOURT
    9     295   13.4    1721  29  AY406082            AY406082 Mus muscu
   10   281.8   12.8     934  13  BU526699            BU526699 AGENCOURT
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   12   272.2   12.4     560  12  BM794145            BM794145 K-EST0075
   13   272.2   12.4     601  12  BM697499            BM697499 UI-E-DX0-
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c  15   270.6   12.3     815   9  AI934968            AI934968 wd17a07.x
   16   269.6   12.3     990  13  BQ071614            BQ071614 AGENCOURT
   17   269.2   12.2     857  13  BU527897            BU527897 AGENCOURT
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   24   264.2   12.0     851  13  BQ230423            BQ230423 AGENCOURT
   25   264.2   12.0    1622  29  AY406081            AY406081 Pan trogl
   26   263.6   12.0     826  12  BG828886            BG828886 602752869
   27     263   12.0     777  10  BE795217            BE795217 601592482
c  28     258   11.7     713  10  AW173009            AW173009 xj82a11.x
   29     258   11.7    1057  13  BQ071329            BQ071329 AGENCOURT
   30     256   11.6     543  10  BE394617            BE394617 601311853
   31   254.8   11.6     707  12  BG823182            BG823182 602726540
c  32   253.6   11.5     769  13  BW013848            BW013848 BW013848
   33   252.8   11.5     892  14  CB195631            CB195631 AGENCOURT
   34   252.4   11.5     838  13  BX849055            BX849055 BX849055
c  35   250.2   11.4     810  13  BW085647            BW085647 BW085647
c  36     249   11.3     676   9  AI640213            AI640213 wa30e01.x
c  37   247.8   11.3     792  13  BX684426            BX684426 BX684426
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                               ALIGNMENTS


RESULT 1
AK051405
LOCUS       AK051405                2978 bp    mRNA    linear   HTC 20-SEP-2003
DEFINITION  Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
            enriched library, clone:D130046K22 product:G PROTEIN-COUPLED
            RECEPTOR KINASE GRK6 (EC 2.7.1.-) homolog [Mus musculus], full
            insert sequence.
ACCESSION   AK051405
VERSION     AK051405.1  GI:26094516
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
  PUBMED      11042159
REFERENCE     3
  AUTHORS     Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
              Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
              Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
              Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
              Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
              Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
              Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE       RIKEN integrated sequence analysis (RISA) system--384-format
              sequencing pipeline with 384 multicapillary sequencer
  JOURNAL     Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE     20530913
  PUBMED      11076861
REFERENCE     4
  AUTHORS     The RIKEN Genome Exploration Research Group Phase II Team and the
              FANTOM Consortium.
  TITLE       Functional annotation of a full-length mouse cDNA collection
  JOURNAL     Nature 409, 685-690 (2001)
REFERENCE     5
  AUTHORS     The FANTOM Consortium and the RIKEN Genome Exploration Research
              Group Phase I & II Team.
  TITLE       Analysis of the mouse transcriptome based on functional annotation
              of 60,770 full-length cDNAs
  JOURNAL     Nature 420, 563-573 (2002)
REFERENCE     6  (bases 1 to 2978)
  AUTHORS     Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
              Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
              Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
              Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
              Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
              Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
              Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
              Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
              Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
              Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
              Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
              Muramatsu,M. and Hayashizaki,Y.
  TITLE       Direct Submission
  JOURNAL     Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
              Physical and Chemical Research (RIKEN), Laboratory for Genome
              Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
              RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
              Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
              URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
              Fax:81-45-503-9216)
COMMENT       cDNA library was prepared and sequenced in Mouse Genome
              Encyclopedia Project of Genome Exploration Research Group in Riken
              Genomic Sciences Center and Genome Science Laboratory in RIKEN.
              Division of Experimental Animal Research in Riken contributed to
              prepare mouse tissues.
              Please visit our web site for further details.
              URL:http://genome.gsc.riken.go.jp/
              URL:http://fantom.gsc.riken.go.jp/.
FEATURES               Location/Qualifiers
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                       /dev_stage="12 days embryo"
     misc_feature      256. .1893
                       /note="G PROTEIN-COUPLED RECEPTOR KINASE GRK6 (EC 2.7.1.-)
                       homolog [Mus musculus] (SWISSPROT|O70293, evidence: FASTY,
                       100%ID, 96.9%length, match=1714)
                       putative"
ORIGIN
```

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  Query Match             18.1%;  Score 398.6;  DB 11;  Length 2978;
  Best Local Similarity   55.5%;  Pred. No. 3.3e-77;
  Matches  832;  Conservative    0;  Mismatches  659;  Indels    8;  Gaps    3;

Qy        388 GGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGT 447
              |||| |  |  |||    ||||    |       || | |||||| || |  |  ||  
Db        248 GGCGCCAGATGCTGCAGTTCCCCCATATCAGCCAGTGTGAGGAGCTTCGACTCAGCCTTG 307

Qy        448 CCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACT 507
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Qy        508 TCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACT 567
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Db        368 TCTGTGCTACGAGACCTGAGCTGACCCGGTGTACTGCCTTCCTGGATGGGGTGTCTGAAT 427

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Qy        628 GTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCA 687
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Qy        688 AGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTG 747
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Qy        868 AGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACA 927
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Qy        928 CTGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCG 987
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Qy        988 AGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCT 1047
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Db        1440 ACCCTGCTGAGCGCCTGGGGTGTCGTGGAGGTGGCGCCCGTGAGGTAAAGGAGCACCCCC 1499

Qy        1648 TCTTTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGC 1707
               | || || |   | || ||    || |||| ||||||| |  | || || || |||  ||
Db        1500 TTTTCAAGAAACTGAATTTCAAGCGGCTGGGAGCTGGCATGCTAGAGCCACCTTTTAAGC 1559

Qy        1708 CAGACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTC 1767
               | || ||    |   |||||  ||| ||  ||   || |||||  | ||||||   |||
Db        1560 CTGATCCCCAGGCTATTTATTGCAAGGATGTCCTGGACATTGAACAGTTCTCTACAGTTA 1619

Qy        1768 GGGGGGTGGAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTG 1827
                 || |||||  | ||   || |||  |  | |||| | | || ||||| |||||   ||
Db        1620 AAGGTGTGGATCTGGAGCCCACAGACCAAGACTTCTACCAGAAGTTTGCCACAGGCAGTG 1679

Qy        1828 TTCCTATAGCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGAC 1886
               |  | ||  | |||||| | || ||  | || || |     ||  ||||||| |||| |
Db        1680 TGTCCATCCCCTGGCAGAATGAGATGGTGGAGACCGAGTGCTTCCAGGAACTCAATGTC 1738

RESULT 2
BC057206
LOCUS       BC057206                2989 bp    mRNA    linear   HTC 19-NOV-2003
DEFINITION  Mus musculus G protein-coupled receptor kinase 6, mRNA (cDNA clone
            IMAGE:5328461), containing frame-shift errors.
ACCESSION   BC057206
VERSION     BC057206.1  GI:34784381
KEYWORDS    HTC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2989)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 2989)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-AUG-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
            Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 123 Row: m Column: 10
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 7242151
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="NMRI"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5328461"
                     /tissue_type="Mammary tumor. WAP-Tag model. 5 months old,
                     gross tissue."
                     /clone_lib="NCI_CGAP_Mam4"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
ORIGIN

  Query Match             17.1%;  Score 376;  DB 11;  Length 2989;
  Best Local Similarity   54.8%;  Pred. No. 3.3e-72;
  Matches  883;  Conservative    0;  Mismatches  700;  Indels   27;  Gaps    6;

Qy         280 CGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACC 339
               || ||   ||   | || |      ||  || || ||| |  | || ||||| |     |
Db         145 CGGGCCGGGCGGCGCTGCAGCCCATGGAGCTCGAGAACATCGTAGCGAACACGGTGCTAC 204

Qy         340 TGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTA 396
               |  |||||||| |       | | |  |  ||||||   ||    ||    |||| |  |
Db         205 TCAAGGCCCGGGAAGGTGGTGGCGGGAATCGCAAAGGCAAGAGCAAGAAATGGCGCCAGA 264

Qy         397 GCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACT 456
                 |||    | |||    |       || | |||||| || |  |  ||    |   |||
Db         265 TGCTGCAGTTCCCCCATATCAGCCAGTGTGAGGAGCTTCGACTCAGCCTTGAGCGTGACT 324

Qy         457 TCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCA 516
                ||||||||| |||||||  |||||||| || ||||   | || ||||| |||   || |
Db         325 ACCACAGCCTATGTGAGCGCCAGCCCATTGGGCGCCTGTTATTTCGTGAGTTCTGTGCTA 384

Qy         517 CAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGG 576
               |    ||   | |   |  |    |  ||||||| || |  |||    | |  ||| ||
Db         385 CGAGACCTGAGCTGACCCGGTGTACTGCCTTCCTGGATGGGGTGTCTGAATATGAGGTGA 444

Qy         577 CCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTG 636
               ||   || |        ||||   | | ||  |   | ||  ||   |  | |  |||
Db         445 CCCCTGATGAGAAGCGGAAAGCATGTGGGCGCC---GACTAATGCAGAACTTTCTGAGCC 501

Qy         637 CCCCTGCCCCGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAG 696
                | | |  || |    |   |      | |   | |||   |||   | |  ||||| ||
Db        502 ACACGGGTCCTGACCTCATCCCTGAAGTTCCACGGCAGCTGGTGAGTAAC-TGTGCCCAG 560

Qy        697 CAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGG 756
              | || |   | | |     || |    ||              |  ||||||  ||   |
Db        561 CGGCTAGAGCAGGGACCCTGCAAAGACCTCTTCCAGGAGCTGACCCGGCTGA--CCCACG 618

Qy        757 CTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTC 816
                | | ||     |   || |||   || | | |   ||||  || || |  ||   ||||
Db        619 AGTACCTGAGCACGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAACCGTTTTC 678

Qy        817 TGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAG 876
              ||||||||||     | || | |||||||||| |  | ||   |||||   ||| | |||
Db        679 TGCAGTGGAAGTGGCTGGAAAGGCAACCAGTGACCAAAAACACCTTCAGGCAGTACCGAG 738

Qy        877 TGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGA 936
              | ||||| ||||||| |||||||||||  | ||                || || ||||
Db        739 TCCTGGGCAAAGGTGGCTTTGGGGAGGTGCGGGCA---------------ACAGGCAAGA 783

Qy        937 TGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAAGGTGGCGAGAAGATGG 996
              |||| || || ||||||||||| |||||||||| | ||||||  |   || |||   ||||
Db        784 TGTACGCATGCAAGAAACTGGAAAAGAAGCGGATAAAGAAGCGAAAGGGGGAGGCCATGG 843

Qy        997 CTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCT 1056
              |||||   || ||  | ||||||||||| || | |||    ||  | ||     | ||||
Db        844 CTCTCAACGAGAAACAGATCTTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTTAGCCT 903

Qy       1057 ATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACC 1116
              | |||| ||||| ||||      || ||||| ||  |||     |||||||||| || ||||
Db        904 ACGCCTATGAGACCAAGGATGCACTGTGCCTGGTGCTGACATTGATGAATGGAGGTGACC 963

Qy       1117 TCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTT 1176
              | ||||||||||||||| || |||||  |  |||| |          || |   |||| |
Db        964 TAAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTTCCTGAAGCACGTGCTGTCTTCT 1023

Qy       1177 ACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGG 1236
              |  | ||  ||||   ||||||  ||    |||| ||        |||| || ||  |||
Db       1024 ATGCTGCTGAGATCTGCTGTGGCCTGGAAGACCTGCACCGGGAACGCATTGTGTACAGGG 1083

Qy       1237 ACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGG 1296
              |  | ||||| |||||| | |||||||||||||  ||| ||    || | || |||||||
Db       1084 ATCTAAAGCCAGAGAATATCCTTCTGGATGACCATGGCCACATTCGGATCTCGGACCTGG 1143

Qy       1297 GGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTT 1356
              | ||||||||| |  ||   |  ||| || ||||||      | |  || ||    || |
Db       1144 GACTGGCCGTGCATGTGCCTGAGGGCCAGACCATCAAAGGCCGTGTGGGCACTGTGGGCT 1203

Qy       1357 ACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTG 1416
              |||||||||| ||| |  | | |   || |   | ||  | |    |   |||||||  |
Db       1204 ACATGGCTCCAGAGGTGGTGAGG---AATGAGCGCTACACGTTCAGTCCTGACTGGTGGG 1260

Qy       1417 CCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGG 1476
              |  | || ||  | | || || ||| | || || |   | || ||| |  |    |||
Db       1261 CGCTAGGCTGCCTCCTGTACGAGATGATCGCAGGTCAGTCGCCCTTCCAGCAGAGGAAGA 1320

Qy       1477 AAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGC 1536
              | ||| | |     || ||  || |||          | |||  |  |   | | |
Db       1321 AGAAGATAAAGCGCGAAGAGGTGGAGCGGCTGGTCAAGGAAGTGGCCGAGGAGTACACAG 1380

Qy       1537 ATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAG 1596
              |       | | || |||       |      ||    |||  |         |     | |
Db       1381 ACCGCTTTTCCTCACAGGCGCGCTCACTCTGTTCTCAGCTTCTTAGCAAGGACCCTGCTG 1440

Qy       1597 AGCAACGCTTAGGAAGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAA 1656
              |||  |       |  |  |||      |   |||    | | | || |   | || || |
Db       1441 AGCGCCTGGGGTGTCGTGGAGGTGGCGCCCGTGAGGTAAAGGAGCACCCCCTTTTCAAGA 1500

Qy       1657 CGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTT 1716
                 | || ||    || ||||| ||||||| |  | || || || |||  ||| || ||
Db       1501 AACTGAATTTCAAGCGGCTGGGAGCTGGCATGCTAGAGCCACCTTTTAAGCCTGATCCCC 1560

Qy       1717 CAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGG 1776
                |   |||||  ||| ||  ||   || |||||  | ||||||   |||   || ||||
Db       1561 AGGCTATTTATTGCAAGGATGTCCTGGACATTGAACAGTTCTCTACAGTTAAAGGTGTGG 1620
```

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Qy       1777 AATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAG 1836
              |  | ||   || |||  |  | |||| | | || |||||  |||||   |||  | ||
Db       1621 ATCTGGAGCCCACAGACCAAGACTTCTACCAGAAGTTTGCCACAGGCAGTGTGTCCATCC 1680

Qy       1837 CATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGAC 1886
              | |||||| | || ||  | || || |     ||  |||||||| |||| |
Db       1681 CCTGGCAGAATGAGATGGTGGAGACCGAGTGCTTCCAGGAACTCAATGTC 1730


RESULT 3
BX404586/c
LOCUS       BX404586                1201 bp    mRNA    linear   EST 13-MAY-2003
DEFINITION  BX404586 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
            CS0DA004YM05 3-PRIME, mRNA sequence.
ACCESSION   BX404586
VERSION     BX404586.1  GI:30648023
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 3090.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0AA004AG03NP1&cluster=3090.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0AA004AG03NP1.
FEATURES             Location/Qualifiers
     source          1..1201
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                     /clone="CS0DA004YM05"
                     /tissue_type="NEUROBLASTOMA"
                     /clone_lib="Homo sapiens NEUROBLASTOMA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match             14.2%;  Score 311.8;  DB 13;  Length 1201;
  Best Local Similarity   59.8%;  Pred. No. 4.6e-58;
  Matches  539;  Conservative    1;  Mismatches  358;  Indels    3;  Gaps    1;

Qy        812 GTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTT 871
              :|| ||||||||||||     | || | ||| |||||| |  | ||   |||||   | |
Db       1004 KTTCCTGCAGTGGAAGTGGCTGGAAARGCAGCCAGTGACCAAAAACACCTTCAAGCAATA 945

Qy        872 CAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGG 931
              | |||| ||||| ||||||||| |||||||||||| || |||  |||||||     ||| ||
Db        944 CCGAGTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGG 885

Qy        932 GAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAA 991
               |||||||||||||| |||||| || || || |||||| | ||||||      || |||
Db        884 TAAGATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAGGC 825

Qy        992 GATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCT 1051
               ||||| ||    || ||| | ||| |||||||| || | |||    ||  | ||     |
Db        824 CATGGCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTT 765
```

```
Qy   1052 GGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGG 1111
          |||||| |||| ||||| ||||  |   || ||||| ||  |||  |||||||| |||||
Db    764 GGCCTACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGG 705

Qy   1112 AGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGAT 1171
           ||||||||||||||||||||| || |||||  |  |||| |   |      ||||   |
Db    704 CGACCTCAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGCCGT 645

Qy   1172 CTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTA 1231
          ||| ||| | ||| ||||   ||||||  ||  | |||| ||        ||||||| ||
Db    644 CTTCTACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTA 585

Qy   1232 TCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGA 1291
            ||||| ||||||| |||||  |  | |||||||||| |||| ||  | |  | |||||
Db    584 CAGGGACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTCTGA 525

Qy   1292 CCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAA 1351
          |||||| || || ||| |  ||   |  ||| || ||||||    | | |  || |||
Db    524 CCTGGGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGT 465

Qy   1352 TGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTG 1411
           |||||||||||||| |||    |  || | || | | | ||  | |        |||||
Db    464 GGGTTACATGGCTCCGGAG---GTGGTGAAGAATGAACGGTACACGTTCAGCCCTGACTG 408

Qy   1412 GTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTA 1471
          ||  ||  | || |||  | | || || ||| | || || |   | || ||| |  |
Db    407 GTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCAGAG 348

Qy   1472 CAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATT 1531
           ||| | ||| |||     |||||  || |||          | | | |   |   | |
Db    347 GAAGAAGAAGATCAAGCGGGAGGAGGTGGAGCGGCTGGTGAAGGAGGTCCCCGAGGAGTA 288

Qy   1532 CCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAA 1591
               |       | | |  |||       |  |   |    ||||  |||      |
Db    287 TTCCGAGCGCTTTTCCCCGCAGGCCCGCTCACTTTGCTCACAGCTCCTCTGCAAGGACCC 228

Qy   1592 ACCAGAGCAACGCTTAGGAAGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTT 1651
            | || |  |      |  |  | |  |   |    ||    | | | || |   ||||
Db    227 TGCCGAACGCCTGGGGTGTCGTGGGGGCAGTGCCCGCGAGGTGAAGGAGCACCCCCTCTT 168

Qy   1652 TAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGA 1711
          ||| | | | |||||    || |||| ||||||| |  | || || || ||   ||| ||
Db    167 TAAGAAGCTGAACTTCAAGCGGCTGGGAGCTGGCATGCTGGAGCCGCCCTTCAAGCCTGA 108

Qy   1712 C 1712
          |
Db    107 C 107


RESULT 4
BC027597
LOCUS       BC027597               2329 bp    mRNA    linear   HTC 01-MAY-2002
DEFINITION  Homo sapiens, Similar to G protein-coupled receptor kinase 2-like
            (Drosophila), clone IMAGE:4830673, mRNA.
ACCESSION   BC027597
VERSION     BC027597.1  GI:20379554
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2329)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) &  Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 34 Row: i Column: 14
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4885346
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4830673"
                     /tissue_type="Testis"
                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript"
ORIGIN

  Query Match             14.2%;  Score 311.6;  DB 11;  Length 2329;
  Best Local Similarity   57.4%;  Pred. No. 5.9e-58;
  Matches  623;  Conservative    0;  Mismatches  454;  Indels    9;  Gaps    3;

Qy    767 AGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAA 826
          || | | || ||| | || | |      ||| | |  |      ||||| | ||  |||||
Db    921 AGGGGAACCATTTGAAGAATACCAAGAAAGCTCATATTTTTCTCAGTTTTACAATGGAA 980

Qy    827 ACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAA 886
          |    | || | |||||| ||  || | ||    || |   | | |||||| || || ||
Db    981 ATGGCTGGAAAGGCAACCCGTAACAAAGAACACATTTAGACATTACAGAGTTCTAGGAAA 1040

Qy    887 AGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTG 946
          ||| || ||||| ||||| || |||   || |||  |  ||| || || |||||||||||
Db   1041 AGGCGGATTTGGAGAGGTTTGCGCCTGTCAAGTGCGAGCCACAGGAAAAATGTATGCCTG 1100

Qy    947 TAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGA 1006
           || || ||  | || ||  |  | |||||||     || ||    ||||||||    ||
Db   1101 CAAAAAGCTACAAAAAAAAAGAATAAAGAAGAGGAAAGGTGAAGCTATGGCTCTAAATGA 1160

Qy   1007 AAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGA 1066
           ||   |||  ||||||| ||    ||    ||| | ||   | | ||||| || | |||
Db   1161 GAAAAGAATTCTGGAGAAAGTGCAAAGTAGATTCGTAGTTAGTTTAGCCTACGCTTATGA 1220

Qy   1067 GAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCA 1126
           | |||        | ||| | ||  | | | | |||||||| || ||  | ||||| ||
Db   1221 AACCAAAGATGCCTTGTGCTTGGTGCTCACCATTATGAATGGAGGGGATTTGAAGTTTCA 1280

Qy   1127 CATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCA 1186
          ||| |||||| ||||||  |  ||| | ||   |    | |   | || ||  | ||  |
Db   1281 CATTTACAACCTGGGCAATCCCGGCTTTGATGAGCAGAGAGCCGTTTTCTATGCTGCAGA 1340

Qy   1187 GATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCC 1246
          | |    || ||  ||    |  | ||        | || || ||  | ||| |||||||
Db   1341 GCTGTGTTGCGGCTTGGAAGATTTACAGAGGGAAAGAATTGTATACAGAGACTTGAAGCC 1400

Qy   1247 TGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGT 1306
          ||||||| | || || ||||| |  ||  ||  | || | || ||||| ||  |||||
Db   1401 TGAGAATATTCTCCTTGATGATCGTGGACACATCCGGATTTCAGACCTCGGTTTGGCCAC 1460

Qy   1307 GGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCC 1366
           |||||    |  ||  ||    |       || | ||||||    || |||||||| ||
Db   1461 AGAGATCCCAGAAGGACAGAGGGTTCGAGGAAGAGTTGGAACAGTCGGCTACATGGCACC 1520

Qy   1367 TGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATG 1426
          |||  |  | |   | || | ||  ||| | | |  |   || ||||  |   | || ||
Db   1521 TGAAGTTGTCA---ATAATGAAAAGTATACGTTTAGTCCCGATTGGTGGGGACTTGGCTG 1577
```

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Qy       1427 CAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAG 1486
                  || ||||||||| ||   ||||   | ||||||||| | ||||| || || ||||
Db       1578 TCTGATCTATGAAATGATTCAGGGACATTCTCCATTCAAAAAATACAAAGAGAAAGTCAA 1637

Qy       1487 TAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTT 1546
                  |||||  |  | |||||||   |  |  | ||   | |     |   ||| || ||
Db       1638 ATGGGAGGAGGTCGATCAAAGAA---TCAAGAATGATACCGAGGAGTATTCTGAGAAGTT 1694

Qy       1547 CACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTT 1606
                ||||||| || |||  ||| |||||| | ||  |  | ||||| |||    | ||  |
Db       1695 TTCAGAGGATGCCAAATCTATCTGCAGGATGTTACTCACCAAGAATCCAAGCAAGCGGCT 1754

Qy       1607 AGGAAGCAGAGAAAAG---TCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAA 1663
               ||  |||| |   ||    | | ||     | | | || |   | || ||    |||||
Db       1755 GGGCTGCAGGGGCGAGGGAGCGGCTGGGGTGAAGCAGCACCCCGTGTTCAAGGACATCAA 1814

Qy       1664 CTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGT 1723
              |||     | ||||| ||   | |  | || ||||| ||    || || |||   |  ||
Db       1815 CTTCAGGAGGCTGGAGGCAAACATGCTGGAGCCCCCTTTCTGTCCTGATCCTCATGCCGT 1874

Qy       1724 TTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGA 1783
              |||    || ||| ||   || || ||  | ||||| | |||    ||| |  |  | ||
Db       1875 TTACTGTAAGGACGTCCTGGATATCGAGCAGTTCTCGGCGGTGAAAGGGATCTACCTGGA 1934

Qy       1784 TGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCA 1843
                 |  |||| |  | ||||        ||||| || ||   |||  | ||  | |||||
Db       1935 CACCGCAGATGAAGACTTCTATGCTCGGTTTGCTACCGGGTGTGTCTCCATCCCCTGGCA 1994

Qy       1844 GGAAGA 1849
              | | ||
Db       1995 GAATGA 2000


RESULT 5
BX392018/c
LOCUS       BX392018                 917 bp    mRNA    linear   EST 13-MAY-2003
DEFINITION  BX392018 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL010YD11 3-PRIME, mRNA sequence.
ACCESSION   BX392018
VERSION     BX392018.1  GI:30607809
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 917)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 3090.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAI046ZH12_CS04416_1&cluster=3090.f.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAI046ZH12_CS04416_1.
FEATURES             Location/Qualifiers
     source          1..917
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DL010YD11"
                     /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                     /cell_line="RAMOS CELL LINE"
                     /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                     25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             14.0%;  Score 307;  DB 13;  Length 917;
  Best Local Similarity   63.8%;  Pred. No. 5e-57;
  Matches  482;  Conservative    0;  Mismatches  270;  Indels    3;  Gaps    1;

Qy        749 GGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGA 808
              | ||    | | | ||   | |   || ||   || | | |   |||||  || || | |
Db        796 GACCCACGAGTACCTGAGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAA 737

Qy        809 CAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGA 868
              |   || |||||||||||     | || | ||| |||||| |  | ||   |||||   |
Db        736 CCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCA 677

Qy        869 GTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACAC 928
               | | |||| ||||| |||||||| ||||||||||||| || |||  |||||||     |||
Db        676 ATACCGAGTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCAC 617

Qy        929 TGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGA 988
               || |||||||||||||| ||||| || || || |||||| | ||||||      || ||
Db        616 AGGTAAGATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGA 557

Qy        989 GAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTC 1048
              |   ||||| ||    || ||| | ||| |||||| || | |||    ||  | ||   
Db        556 GGCCATGGCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAG 497

Qy       1049 TCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGG 1108
                ||||||| |||| ||||| ||||  |   || ||||| ||  |||  |||||||| ||
Db        496 CTTGGCCTACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGG 437

Qy       1109 GGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGT 1168
              ||| ||||||||||||||||||||||| || ||||  |  |||| |   |      |||| 
Db        436 GGGCGACCTCAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGC 377

Qy       1169 GATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGT 1228
                |||| ||| | ||| ||||   ||||||  ||  | |||| ||        |||||||
Db        376 CGTCTTCTACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGT 317

Qy       1229 CTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATC 1288
               ||  ||||| ||||||| |||||  |  | |||||||||| |||| |   | |    ||
Db        316 GTACAGGGACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTC 257

Qy       1289 TGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAAC 1348
              ||||||||| || || ||| |  ||   |  ||| || ||||||    | | |  || ||
Db        256 TGACCTGGGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCAC 197

Qy       1349 CAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGA 1408
              |   |||||||||||||| |||    |  || | || | | | ||    |        ||
Db        196 CGTGGGTTACATGGCTCCGGAG---GTGGTGAAGAATGAACGGTACACGTTCAGCCCTGA 140

Qy       1409 CTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGA 1468
              |||||  ||  | || |||  | | || || |||   || || |   |  | ||| |  |
Db        139 CTGGTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCA 80

Qy       1469 TTACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGC 1503
                  ||| | ||| |||     |||||  || |||
Db         79 GAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGAGC 45


RESULT 6
AY406080
LOCUS       AY406080                1721 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens GPRK5 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406080
VERSION     AY406080.1  GI:39762054
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1721)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1721)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..1721
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1..>1721
                     /gene="GPRK5"
                     /locus_tag="HCM2438"
ORIGIN

  Query Match             13.9%;  Score 304.6;  DB 29;  Length 1721;
  Best Local Similarity   49.5%;  Pred. No. 2e-56;
  Matches  559;  Conservative    0;  Mismatches  561;  Indels    9;  Gaps    3;

Qy        759 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 818
              | | ||   |   | || ||  | || |   ||  ||||   || |  |||   |||||
Db        402 TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTTGACCGCTTTCTC 461

Qy        819 CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 878
              ||||||||    || || |
Db        462 CAGTGGAAGTGGTTGGAAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 521

Qy        879 CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG 938
                                      || ||||||  ||||||      ||| || || |||
Db        522 NNNNNNNNNNNNNNNNNNNNNNNNGTCTGTGCCTGCCAGGTTCGGGCCACGGGTAAAATG 581

Qy        939 TATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCT 998
              |||||||| |||    |||| |||||| || | || ||||     || |||   |||||
Db        582 TATGCCTGCAAGCGCTTGGAGAAGAAGAGGATCAAAAAGAGGAAAGGGGAGTCCATGGCC 641

Qy        999 CTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTAT 1058
              |||   || ||| | ||| | |||||||||| ||| |  ||  | |||   |||||||||
Db        642 CTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCCTAT 701

Qy       1059 GCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTC 1118
              ||||  |||| ||||      || ||| | ||| ||| | | ||||||||||| |||||
Db        702 GCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGACCTG 761

Qy       1119 AAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTAC 1178
              |||||||||||||||||| ||||||  | |||| | ||   |   ||||   | |||||
Db        762 AAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTTTAT 821

Qy       1179 TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 1238
               ||||  ||||   ||| ||  |     |||||||         || |||||| || ||
Db        822 GCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGAGAT 881

Qy       1239 ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1298
               |||| ||||| ||  | ||  | |||||    ||| ||   ||| | || ||||||||
Db        882 CTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTGGGC 941

Qy       1299 CTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTAC 1358
               |||| ||| ||||    |  ||  | |  |||  |    |||  || ||   ||| |||
Db        942 TTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGCACTGTTGGCTAC 1001

Qy       1359 ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1418
              |||||||| ||| |||   || | ||    || ||   |         ||||  |  | |
Db       1002 ATGGCTCCAGAGGTCC---TGAACAACCAGAGGTACGGCCTGAGCCCCGACTACTGGGGC 1058

Qy       1419 ATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAA 1478
               | || |||  ||| ||||| ||| | |  || |   | || |||   |    ||||||
Db       1059 CTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCAAGGAG 1118

Qy       1479 AAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCAT 1538
              ||||| |     |||||  || | |   |    ||| |    ||||     | |   ||
Db       1119 AAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGGAGGAGGTGTACTCCCAC 1178

Qy       1539 GATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAG 1598
                 || ||| | ||||| || ||    || |||| | |  |  |  | ||  |  |  ||
Db       1179 ---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACGAAAGATGCGAAG 1235

Qy       1599 CAACGCTTAGGAAGCAGAGAAAA---GTCTGATGATCCCAGGAAACATCATTTCTTTAAA 1655
              ||  |  | ||  ||   ||  |   | |||  ||   || || ||| |  ||||| |
Db       1236 CAGAGGCTGGGCTGCCAGGAGGAGGGGGCTGCAGAGGTCAAGAGACACCCCTTCTTCAGG 1295

Qy       1656 ACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCT 1715
              |  || |||||    ||| | ||||| ||  |  | || || || || || ||||||
Db       1296 AACATGAACTTCAAGCGCTTAGAAGCCGGGATGTTGGACCCTCCCTTCGTTCCAGACNNN 1355

Qy       1716 TCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTG 1775

Db       1356 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1415

Qy       1776 GAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATA 1835

Db       1416 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1475

Qy       1836 GCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATG 1884
                             || |||||||| | |   ||| |||| ||||| |
Db       1476 NNNNNNNNNNNNNNNATGATAGAAACAGAATGCTTTAAGGAGCTGAACG 1524


RESULT 7
BQ057469
LOCUS       BQ057469                1058 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6739297 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813090
            5', mRNA sequence.
ACCESSION   BQ057469
VERSION     BQ057469.1  GI:19816809
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1058)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2064  row: j  column: 03
            High quality sequence stop: 631.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5813090"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_99"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match             13.7%;  Score 300.2;  DB 13;  Length 1058;
  Best Local Similarity   63.9%;  Pred. No. 1.7e-55;
  Matches  471;  Conservative    0;  Mismatches  263;  Indels    3;  Gaps    1;

Qy        749 GGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGA 808
              | ||   |  | | ||   | |   || |||   || | | |   ||||  || || | |
Db          5 GACCCACGAGTACCTGAGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAA 64

Qy        809 CAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGA 868
              |   || |||||||||||     | || | ||| |||||| |  | ||   |||||   |
Db         65 CCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCA 124

Qy        869 GTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACAC 928
               | | |||| ||||| |||||||| ||||||||||| || |||  |||||||     |||
Db        125 ATACCGAGTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCAC 184

Qy        929 TGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGA 988
               || |||||||||||||| ||||| || || || |||||| | ||||||      || ||
Db        185 AGGTAAGATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGA 244

Qy        989 GAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTC 1048
              |   ||||| ||    || ||| | ||| ||||||| || | |||    ||  | ||   
Db        245 GGCCATGGCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAG 304

Qy       1049 TCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGG 1108
                ||||||| |||| ||||| ||||  |   || ||||| ||  |||  |||||||| ||
Db        305 CTTGGCCTACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGG 364

Qy       1109 GGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGT 1168
              ||| ||||||||||||||||||||| || |||||  |  |||| |   |      |||| 
Db        365 GGGCGACCTCAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGC 424

Qy       1169 GATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGT 1228
                |||| ||| | ||| ||||   ||||||  ||  | |||| ||        |||||||
Db        425 CGTCTTCTACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGT 484

Qy       1229 CTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATC 1288
               ||  ||||| ||||||| |||||  |  | |||||||||| |||||    | |  | ||
Db        485 GTACAGGGACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTC 544

Qy       1289 TGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAAC 1348
              ||||||||| || || ||| |  ||   |  ||| || ||||||    | | |  || ||
Db        545 TGACCTGGGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCAC 604

Qy       1349 CAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGA 1408
              |   |||||||||||||| |||    |  || | || | | | ||  | |        ||
Db        605 CGTGGGTTACATGGCTCCGGAG---GTGGTGAAGAATGAACGGTACACGTTCAGCCCTGA 661

Qy       1409 CTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGA 1468
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Db        662 CTGGTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAAGCCAGTCGCCCTTCCAGCA 721

Qy       1469 TTACAAGGAAAAGGTCA 1485
                  ||| | ||| |||
Db        722 GAGGAAGAAGAAGATCA 738

RESULT 8
BQ061148
LOCUS       BQ061148                1019 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6862941 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920180
            5', mRNA sequence.
ACCESSION   BQ061148
VERSION     BQ061148.1  GI:19884933
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2083  row: h  column: 05
            High quality sequence stop: 704.
FEATURES             Location/Qualifiers
     source          1..1019
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5920180"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_99"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match             13.6%;  Score 299.2;  DB 13;  Length 1019;
  Best Local Similarity   63.8%;  Pred. No. 2.7e-55;
  Matches  470;  Conservative    0;  Mismatches  264;  Indels    3;  Gaps    1;

Qy        749 GGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGA 808
              | ||   |  | | ||   | |   || |||   || | | |   ||||  || || | |
Db          5 GACCCACGAGTACCTGAGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAA 64

Qy        809 CAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGA 868
              |   || |||||||||||     | || | ||| |||||| |  | ||   |||||   |
Db         65 CCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCA 124

Qy        869 GTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACAC 928
               | | |||| ||||| |||||||| ||||||||||| || |||  |||||||     |||
Db        125 ATACCGAGTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCAC 184

Qy        929 TGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGA 988
               || |||||||||||||| ||||| || || || |||||| | ||||||      || ||
Db        185 AGGTAAGATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGA 244

Qy        989 GAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTC 1048
              |   ||||| ||    || ||| | ||| ||||||| || | |||    ||  | ||   
Db        245 GGCCATGGCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAG 304

Qy       1049 TCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGG 1108
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Db        305 CTTGGCCTACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGG 364

Qy       1109 GGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGT 1168
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Db        365 GGGCGACCTCAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGC 424

Qy       1169 GATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGT 1228
                |||| ||| | ||| ||||   ||||||  ||  | |||| ||        |||||||
Db        425 CGTCTTCTACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGT 484

Qy       1229 CTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATC 1288
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Db        485 GTACAGGGACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTC 544

Qy       1289 TGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAAC 1348
              ||||||| | || || ||| |  ||   |  ||| || ||||||    | | |  || ||
Db        545 TGACCTGNGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCAC 604

Qy       1349 CAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGA 1408
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Db        605 CGTGGGTTACATGGCTCCGGAG---GTGGTGAAGAATGAACGGTACACGTTCAGCCCTGA 661

Qy       1409 CTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGA 1468
              |||||  ||  | || |||  | | || || ||| | || || |   | || ||| |  |
Db        662 CTGGTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCA 721

Qy       1469 TTACAAGGAAAAGGTCA 1485
                  ||| | ||  |||
Db        722 GAGGAAGAAGAAAATCA 738

RESULT 9
AY406082
LOCUS       AY406082                1721 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus GPRK5 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406082
VERSION     AY406082.1  GI:39762056
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1721)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1721)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
     source          1..1721
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1..>1721
                     /gene="GPRK5"
                     /locus_tag="HCM2438"
ORIGIN

  Query Match             13.4%;  Score 295;  DB 29;  Length 1721;
  Best Local Similarity   49.0%;  Pred. No. 2.6e-54;
  Matches  553;  Conservative    0;  Mismatches  567;  Indels    9;  Gaps    3;

Qy        759 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 818
              | |||| | |   | |||||  | || | | ||   |||   |  |  |||   ||||||
Db        402 TACTTGAAGGGAGACCCCTTCCACGAGTACCTGGATAGCATGTATTTTGACCGTTTTCTG 461

Qy        819 CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 878
              |||||||||   || || |
Db        462 CAGTGGAAATGGTTAGAAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 521

Qy        879 CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG 938
                                      || ||||||  ||||||      |||||| || |||
Db        522 NNNNNNNNNNNNNNNNNNNNNNNNGTCTGTGCCTGCCAGGTTCGGGCCACTGGTAAAATG 581

Qy        939 TATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCT 998
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Db        582 TATGCTTGTAAACGCTTAGAGAAGAAGAGGATCAAAAAGAGGAAAGGCGAATCCATGGCA 641

Qy        999 CTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTAT 1058
              |||   |||||| | ||  | ||||||||||| |||||  ||  | |||   |||||||||
Db        642 CTCAACGAAAAGCAGATTCTTGAGAAGGTCAACAGCCAGTTTGTGGTCAACCTGGCCTAT 701

Qy       1059 GCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTC 1118
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Db        702 GCCTATGAAACCAAAGATGCACTATGCCTGGTTCTGACCATTATGAATGGTGGTGACCTG 761

Qy       1119 AAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTAC 1178
              ||||| |||||||||||  |||| |  | |||| | ||       || |   | |||||
Db        762 AAGTTTCACATCTACAATATGGGGAATCCTGGCTTTGAGGAAGAGCGAGCCTTATTTTAT 821

Qy       1179 TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 1238
               | ||  ||||   ||||||  |     || | ||         ||  ||||||| | ||
Db        822 GCAGCTGAGATCCTCTGTGGCCTAGAAGACTTACACCGTGAGAACACTGTCTATAGAGAT 881

Qy       1239 ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1298
               | || || || ||  |  | |||||||||    ||| ||   ||| | || ||||| ||
Db        882 CTAAAACCCGAAAACATCTTGCTGGATGATTATGGCCACATAAGGATCTCAGACCTCGGA 941

Qy       1299 CTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTAC 1358
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Db        942 CTGGCCGTGAAGATCCCCGAGGGAGACCTTATCCGTGGCCGGGTAGGCACTGTTGGCTAC 1001

Qy       1359 ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1418
              ||||| || ||  | || |   |  ||  |  |         ||||   |||||   | |
Db       1002 ATGGCCCCAGAAGTTCTGAACAACCAGCGATATGGACTGAGCCCTGACTACTGG---GGC 1058

Qy       1419 ATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAA 1478
               |||| |||  ||| ||||| ||| |||  || |   |||||||   || |   |||||
Db       1059 CTGGGCTGCCTCATCTATGAGATGATTGAAGGCCAGTCACCATTTCGAGGTCGCAAGGAG 1118

Qy       1479 AAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCAT 1538
              ||||| |       || ||  || | |   |    ||| |    ||||   || |  |
Db       1119 AAGGTTAAGCGGGAAGAGGTGGATCGCCGGGTGCTGGAGACTGAGG---AAGTATATTCC 1175

Qy       1539 GATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAG 1598
                 || ||| | || || ||  ||    || ||||   |  |  |  | ||  |  |  ||
Db       1176 TCCAAGTTCTCTGAAGAGGCCAAGTCCATCTGCAACATGCTGCTCACCAAAGACTCGAAG 1235

Qy       1599 CAACGCTTAGGAAGCAGAGAAAA---GTCTGATGATCCCAGGAAACATCATTTCTTTAAA 1655
              ||  |  | ||  ||   ||  |   | | |  ||   || ||  || | |||||| |
Db       1236 CAGAGGCTGGGCTGCCAGGAGGAGGGGGCCGCCGAGGTCAAGAGGCACCCTTTCTTCAGG 1295

Qy       1656 ACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCT 1715
              |  || ||||||   ||||||||| |||||  |  | || || || || || |||||
Db       1296 AACATGAACTTTAAGCGCCTGGAGGCTGGGATGTTGGACCCTCCCTTCGTTCCAGATNNN 1355

Qy       1716 TCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTG 1775

Db       1356 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1415

Qy       1776 GAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATA 1835

Db       1416 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1475

Qy       1836 GCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATG 1884
                             || |||||||| | |   ||  |||| |||||||
Db       1476 NNNNNNNNNNNNNNNATGATAGAAACAGAATGTTTCAAGGAGCTGAATG 1524


RESULT 10
BU526699
LOCUS       BU526699                 934 bp    mRNA    linear   EST 13-SEP-2002
DEFINITION  AGENCOURT_10181837 NIH_MGC_101 Homo sapiens cDNA clone
            IMAGE:6536408 5', mRNA sequence.
ACCESSION   BU526699
VERSION     BU526699.1  GI:22837140
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 934)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2697  row: 1  column: 08
            High quality sequence stop: 640.
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                     /db_xref="taxon:9606"
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                     /tissue_type="epidermoid carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_101"
                     /note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
                     XhoI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             12.8%;  Score 281.8;  DB 13;  Length 934;
  Best Local Similarity   62.6%;  Pred. No. 1.9e-51;
  Matches  455;  Conservative    0;  Mismatches  269;  Indels    3;  Gaps    1;

Qy        759 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 818
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Db         78 TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTTGACCGCTTTCTC 137

Qy        819 CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 878
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Db        138 CAGTGGAAGTGGTTGGAAAGGCAACCGGTGACCAAAAACACTTTCAGGCAGTATCGAGTG 197

Qy        879 CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG 938
              || || ||||| || || |||||||| ||||||  ||||||      ||| || || |||
Db        198 CTAGGAAAAGGGGGCTTCGGGGAGGTCTGTGCCTGCCAGGTTCGGGCCACGGGTAAAATG 257

Qy        939 TATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCT 998
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Db        258 TATGCCTGCAAGCGCTTGGAGAAGAAGAGGATCAAAAAGAGGAAAGGGGAGTCCATGGCC 317

Qy        999 CTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTAT 1058
              |||   || ||| | ||| | |||||||||| ||| |  ||  | |||    |||||||||
Db        318 CTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCCTAT 377

Qy       1059 GCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTC 1118
              ||||  |||| ||||      || ||| | ||| ||| | | |||||||||||| |||||
Db        378 GCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGACCTG 437

Qy       1119 AAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTAC 1178
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Db        438 AAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTTTAT 497

Qy       1179 TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 1238
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Db        498 GCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGAGAT 557

Qy       1239 ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1298
               |||| ||||| ||  | ||  | |||||    ||| ||   ||| | || ||||||||
Db        558 CTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTGGGC 617

Qy       1299 CTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTAC 1358
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Db        618 TTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGNCGGGTGGGCACTGTTGGCTAC 677

Qy       1359 ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1418
              |||||||| ||| |||   || || |    || ||   |         ||||  |  | |
Db        678 ATGGCTCCAGAGGTCC---TGAAACACCAGAGGTACGGCCTGAGCCCCGACTACTGGGGC 734

Qy       1419 ATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAA 1478
               | || |||  ||| ||||| ||| | |  || |   | || |||   |    ||||||
Db        735 CTTGGCTGCCTCATCTATGAGATGATCGAAGGCCAGTCGCCGTTCCGCGGNCGCAAGGAG 794

Qy       1479 AAGGTCA 1485
              || || |
Db        795 AAAGTGA 801


RESULT 11
BU146436
LOCUS       BU146436                 903 bp    mRNA    linear   EST 03-SEP-2002
DEFINITION  AGENCOURT_8728162 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6339126
            5', mRNA sequence.
ACCESSION   BU146436
VERSION     BU146436.1  GI:22659968
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 903)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2533  row: h  column: 07
            High quality sequence stop: 635.
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                     /lab_host="DH10B (phage-resistant)"
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                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
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                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
```

```
                    insert size 1.8kb.  Library constructed by Ling Hong in
                    the laboratory of Gerald M. Rubin (University of
                    California, Berkeley) using ZAP-cDNA synthesis kit
                    (Stratagene) and Superscript II RT (Life Technologies).
                    Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             12.8%;  Score 280.6;  DB 13;  Length 903;
  Best Local Similarity   62.6%;  Pred. No. 3.5e-51;
  Matches  455;  Conservative    0;  Mismatches  269;  Indels    3;  Gaps    1;

Qy        759 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 818
              | | ||   |   | || ||  | || |   ||  ||||   || |  |||   |||||
Db         93 TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTTGACCGCTTTCTC 152

Qy        819 CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 878
              ||||||||    || || | |||||| ||| |  | ||     ||||   |||   |||||
Db        153 CAGTGGAAGTGGTTGGAAAGGCAACCGGTGACCAAAAACACTTTCAGGCAGTATCGAGTG 212

Qy        879 CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG 938
              || || ||||| || || ||||||||| ||||||  |||||||      ||| || || |||
Db        213 CTAGGAAAAGGGGGCTTCGGGGAGGTCTGTGCCTGCCAGGTTCGGGCCACGGGTAAAATG 272

Qy        939 TATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCT 998
              |||||||| |||    |||| |||||| || | || ||||     || |||   |||||
Db        273 TATGCCTGCAAGCGCTTGGAGAAGAAGAGGATCAAAAAGAGGAAAGGGGAGTCCATGGCC 332

Qy        999 CTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTAT 1058
              |||   || ||| | ||| | |||||||||| ||| |  ||  | |||    |||||||||
Db        333 CTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCCTAT 392

Qy       1059 GCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTC 1118
              ||||  |||| ||||      || ||| | ||| ||| | | |||||||||||| |||||
Db        393 GCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGACCTG 452

Qy       1119 AAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTAC 1178
              |||||||||||||||||| ||||||  | |||| | ||   |   ||||     | |||||
Db        453 AAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTTTAT 512

Qy       1179 TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 1238
               ||||  ||||   ||| ||  |     ||||||||         || |||||| || ||
Db        513 GCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGAGAT 572

Qy       1239 ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1298
               |||| ||||| ||  | ||  | |||||    ||| ||   ||| | || ||||||||
Db        573 CTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTGGGC 632

Qy       1299 CTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTAC 1358
               |||| ||| ||||    |  ||  | |  |||  |    |||  || ||   ||| |||
Db        633 TTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGCACTGTTGGCTAC 692

Qy       1359 ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1418
              |||||||| ||| |||   || | ||    || ||   |         ||||  |  | |
Db        693 ATGGCTCCAGAGGTCC---TGAACAACCAGAGGTACGGCCTGAGCCCCGACTACTGGGGC 749

Qy       1419 ATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAA 1478
               | || |||  ||| ||||| ||| | |  || |   | || |||   |    ||||||
Db        750 CTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCAAGGAG 809

Qy       1479 AAGGTCA 1485
              || || |
Db        810 AAAGTGA 816

RESULT 12
BM794145
LOCUS       BM794145                 560 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  K-EST0075316 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-37-D08
            5', mRNA sequence.
ACCESSION   BM794145
VERSION     BM794145.1  GI:19142377
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 560)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 37  row: D  column: 08
            High quality sequence stop: 560.
FEATURES             Location/Qualifiers
     source          1..560
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S22SNU16n1-37-D08"
                     /sex="F"
                     /tissue_type="Ascites"
                     /cell_type="Lymphoblast-like"
                     /cell_line="SNU-16"
                     /lab_host="DH10B"
                     /clone_lib="S22SNU16n1"
                     /note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
                     Site_2: NotI; The S22SNU16 library was contributed by the
                     Soares laboratory and it was constructed as described by
                     Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
                     Research 6(9): 791-806. RNA was prepared from harvested
                     cells of SNU-16 culture. SNU-16 cell was obtained from
                     Korean Cell Line Bank (KCLB). SNU-16 was established from
                     ascitic fluids of Korean patients by Park J.G. et al.
                     (1990), Cancer Res 50: 2773-2780."
ORIGIN

  Query Match             12.4%;  Score 272.2;  DB 12;  Length 560;
  Best Local Similarity   68.0%;  Pred. No. 2.3e-49;
  Matches  379;  Conservative    0;  Mismatches  178;  Indels    0;  Gaps    0;

Qy        816 CTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGA 875
              |||||||||||     | || | ||| |||||| |  | ||   |||||   | | | ||
Db          1 CTGCAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCAATACCGA 60

Qy        876 GTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAG 935
              || ||||| |||||||| ||||||||||| || |||  |||||||     ||| || |||
Db         61 GTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAG 120

Qy        936 ATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATG 995
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Db        121 ATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATG 180

Qy        996 GCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCC 1055
              || ||    || ||| | ||| ||||||| || | |||    ||  | ||     |||||
Db        181 GCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCC 240

Qy       1056 TATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGAC 1115
              || |||| |||||| ||||  |   || |||||| ||  |||  |||||||| ||||| |||
Db        241 TACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGGCGAC 300

Qy       1116 CTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTT 1175
              |||||||||||||||||| || |||||  |  |||| |   |      ||||   ||||
Db        301 CTCAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTC 360

Qy       1176 TACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGG 1235
              ||| | ||| ||||   ||||||  ||  | |||| ||        |||||||| ||  ||
Db        361 TACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTACAGG 420
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Qy       1236 GACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTG 1295
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Db        421 GACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTCTGACCTG 480

Qy       1296 GGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGT 1355
              || || || ||| |  ||   |  ||| || ||||||    | | |  || |||   |||
Db        481 GGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGGGGGT 540

Qy       1356 TACATGGCTCCTGAGAT 1372
              ||||||||||| ||| |
Db        541 TACATGGCTCCGGAGGT 557


RESULT 13
BM697499
LOCUS       BM697499                 601 bp    mRNA    linear   EST 28-FEB-2002
DEFINITION  UI-E-DX0-agn-o-23-0-UI.r1 UI-E-DX0 Homo sapiens cDNA clone
            UI-E-DX0-agn-o-23-0-UI 5', mRNA sequence.
ACCESSION   BM697499
VERSION     BM697499.1  GI:19010757
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 601)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
   MEDLINE  97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1..601
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-DX0-agn-o-23-0-UI"
                     /tissue_type="fetal eyes"
                     /dev_stage="fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-DX0"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-DX0 is a cDNA library containing the following
                     tissue(s): fetal eyes. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is AGAATCAAGA. This library
                     was created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI)."
ORIGIN
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```
  Query Match             12.4%;  Score 272.2;  DB 12;  Length 601;
  Best Local Similarity   67.5%;  Pred. No. 2.3e-49;
  Matches  382;  Conservative    0;  Mismatches  184;  Indels    0;  Gaps    0;

Qy        816 CTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGA 875
              |||||||||||     | || | ||| |||||| |  | ||   |||||   | | | ||
Db          1 CTGCAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCAATACCGA 60

Qy        876 GTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAG 935
              || ||||| |||||||| ||||||||||| || |||  |||||||     ||| || |||
Db         61 GTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAG 120

Qy        936 ATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATG 995
              ||||||||||| ||||| || || || |||||| | ||||||      || |||   |||
Db        121 ATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATG 180

Qy        996 GCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCC 1055
              || ||    || ||| | ||| ||||||| || | |||    ||  | ||     |||||
Db        181 GCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCC 240

Qy       1056 TATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGAC 1115
              || |||| ||||| ||||  |   || ||||| ||  |||  |||||||| ||||| |||
Db        241 TACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGGCGAC 300

Qy       1116 CTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTT 1175
              |||||||||||||||||| || |||||  |  |||| |   |      ||||   ||||
Db        301 CTCAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTC 360

Qy       1176 TACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGG 1235
              ||| | ||| ||||   ||||||  ||  | |||| ||        ||||||| ||  ||
Db        361 TACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTACAGG 420

Qy       1236 GACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTG 1295
              ||| ||||||| |||||  |  | |||||||||| |||| ||  | |  | |||||||||
Db        421 GACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGNCACATCCGCATCTCTGACCTG 480

Qy       1296 GGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGT 1355
              || || || ||| |  ||   |  ||| || ||||||    | | |  || |||   |||
Db        481 GGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTGGGT 540

Qy       1356 TACATGGCTCCTGAGATCCTAATGGA 1381
              ||||||||||| ||| |  | | | |
Db        541 TACATGGCTCCGGAGGTGGTGAAGAA 566


RESULT 14
BQ061150
LOCUS       BQ061150                1017 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6862973 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920182
            5', mRNA sequence.
ACCESSION   BQ061150
VERSION     BQ061150.1  GI:19884936
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1017)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2083  row: h  column: 07
            High quality sequence stop: 697.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5920182"
                     /tissue_type="lymphoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_99"
                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match             12.4%;  Score 272.2;  DB 13;  Length 1017;
  Best Local Similarity   58.8%;  Pred. No. 2.6e-49;
  Matches  526;  Conservative    0;  Mismatches  359;  Indels    9;  Gaps    3;

Qy        994 TGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGG 1053
              |||| |||   || ||| | ||| | |||||||||| ||| |  ||  | |||   ||||
Db          1 TGGCCCTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGG 60

Qy       1054 CCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAG 1113
              |||||||||  |||| ||||      || ||| | ||| ||| | | ||||||||||| |
Db         61 CCTATGCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTG 120

Qy       1114 ACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCT 1173
              |||| |||||||||||||||||| ||||||  | |||| | ||   |   ||||   | |
Db        121 ACCTGAAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGT 180

Qy       1174 TTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATC 1233
              ||||  ||||  ||||   ||| ||  |     |||||||         || |||||| |
Db        181 TTTATGCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACC 240

Qy       1234 GGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACC 1293
              | ||  |||| ||||| ||  | ||  | |||||    ||| ||   ||| | || ||||
Db        241 GAGATCTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACC 300

Qy       1294 TGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATG 1353
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Db        301 TGGGCTTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGCACTGTTG 360

Qy       1354 GTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGT 1413
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Db        361 GCTACATGGCTCCAGAGGTCC---TGAACAACCAGAGGTACGGCCTGAGCCCCGACTACT 417

Qy       1414 TTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACA 1473
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Db        418 GGGGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCA 477

Qy       1474 AGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCC 1533
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Db        478 AGGAGAAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGGAGG---AGGTGT 534

Qy       1534 AGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAAC 1593
              |     | || ||| | ||||| || ||    || |||| | |  |  |    ||  |
Db        535 ACTCCCACAAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACGAAAGATG 594

Qy       1594 CAGAGCAACGCTTAGGAAGCAGAGAAAA---GTCTGATGATCCCAGGAAACATCATTTCT 1650
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Db        595 CGAAGCAGAGGCTGGGCTGCCAGGAGGAGGGGGCTGCAGAGGTCAAGAGACACCCCTTCT 654

Qy       1651 TTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAG 1710
              | |  |  || |||||    ||| | ||||| ||  |  | || || || || || ||||
Db        655 TCAGGAACATGAACTTCAAGCGCTTAGAAGCCGGGATGTTGGACCCTCCCTTCGTTCCAG 714

Qy       1711 ACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGG 1770
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Db        715 ACCCCCGCGCTGTGTACTGTAAGGACGTGCTGGACATCGAGCAGTTCTCCACTGGTGAAG 774

Qy       1771 GGGTGGAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTC 1830
              | ||  |  | ||  ||| |||  |  | |||| |   || ||  | || ||  ||||
Db        775 GCGTCAATCTGGACCACACAGACGACGACTTCTACTCCAAGTTCTCCACGGGCTCTGTGT 834

Qy       1831 CTATAGCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATG 1884
              | ||  ||||     | || || |||||||| | |   ||| |||| ||||| |
Db        835 CCATCCCATGNGCAAACGAGATGATAGAAACAGAATGCTTTAAGGAGCTGAACG 888


RESULT 15
AI934968/c
LOCUS       AI934968                 815 bp    mRNA    linear   EST 17-DEC-1999
DEFINITION  wd17a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:2328372 3' similar to gb:L15388 G PROTEIN-COUPLED RECEPTOR
            KINASE GRK5 (HUMAN);, mRNA sequence.
ACCESSION   AI934968
VERSION     AI934968.1  GI:5673838
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 815)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1030   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 483.
FEATURES             Location/Qualifiers
     source          1. .815
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2328372"
                     /lab_host="DH10B"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo. "
ORIGIN

  Query Match             12.3%;  Score 270.6;  DB 9;  Length 815;
  Best Local Similarity   62.3%;  Pred. No. 5.7e-49;
  Matches  439;  Conservative    0;  Mismatches  263;  Indels    3;  Gaps    1;

Qy        759 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 818
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Db        711 TACTTGAGGGGAGAACCATCCCACGAATATCTGGACAGCATGTTTTNTGACCGCTTTCTC 652

Qy        819 CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 878
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Job time : 3859.13 secs
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                        GenCore version 5.1.6
                Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         August 13, 2004, 13:15:49 ; Search time 114.544 Seconds
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Title:          US-10-044-205A-1
Perfect score:  2198
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Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:      1365418

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
                 Maximum Match 100%
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    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                               SUMMARIES
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  No.    Score    Match Length DB  ID                          Description
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    2   1658.4    75.5    1662  4  US-09-802-117-1              Sequence 1, Appli
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    9    418.2    19.0    2204  1  US-08-221-817-12             Sequence 12, Appl
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                               ALIGNMENTS

RESULT 1
US-09-802-117-5
; Sequence 5, Application US/09802117
; Patent No. 6444456
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/09/802,117
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER: US 60/188,449
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 2249
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-802-117-5

  Query Match             91.4%;  Score 2008.8;  DB 4;  Length 2249;
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; Sequence 1, Application US/09802117
; Patent No. 6444456
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/09/802,117
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER: US 60/188,449
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-802-117-1

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               |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db         421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy         771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy         831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy         891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy         951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
               ||||||||||||||||||||||||||||||||||||||||||
Db        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662


RESULT 3
US-09-738-894A-1
; Sequence 1, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636
;  CURRENT APPLICATION NUMBER: US/09/738,894A
;  CURRENT FILING DATE:  2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Human
US-09-738-894A-1

  Query Match             75.4%;  Score 1657.2;  DB 4;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1659;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy      531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy      591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy      651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy      711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
            |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db      421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy      771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy      831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy      891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy      951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy     1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy     1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy     1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy     1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy     1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy     1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy     1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
            |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db     1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy     1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy     1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy     1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy     1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy     1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy     1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy     1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy     1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy     1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
            ||||||||||||||||||||||||||||||||||||||||||
Db     1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662

RESULT 4
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV
;  CURRENT APPLICATION NUMBER: US/09/964,469
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Human
US-09-964-469-1

  Query Match             75.4%;  Score 1657.2;  DB 4;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1659;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy      291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy      351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy      411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy      471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy      531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
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Qy         591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy         651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy         711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
               |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db         421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy         771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy         831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy         891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy         951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
               |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
               ||||||||||||||||||||||||||||||||||||||||||
Db        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662
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RESULT 5
US-09-802-117-3
; Sequence 3, Application US/09802117
; Patent No. 6444456
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/09/802,117
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER: US 60/188,449
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1062
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-802-117-3

  Query Match             47.6%;  Score 1046.8;  DB 4;  Length 1062;
  Best Local Similarity   99.8%;  Pred. No. 2.7e-248;
  Matches 1048;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy         591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy         651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1340
              ||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1050

RESULT 6
US-09-738-894A-3
; Sequence 3, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636
;  CURRENT APPLICATION NUMBER: US/09/738,894A
;  CURRENT FILING DATE:  2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 36651
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(36651)
;   OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3

  Query Match             39.5%;  Score 867.4;  DB 4;  Length 36651;
  Best Local Similarity   95.1%;  Pred. No. 1.8e-203;
  Matches  895;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          1 GACCCTAAGATGAAGGGACCTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTGCTTTC 60
              ||||||||||||||||||||         ||      |||| |      |||  ||||||
Db       1786 GACCCTAAGATGAAGGGACCAGTGGGGGAGGTGGCCCCGGCAGGTGTCCCAGCAGCTTTC 1845

Qy         61 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGCAGTTCCTGGCGGGCTATACATAGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1846 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGCAGTTCCTGGCGGGCTATACATAGCCA 1905

Qy        121 GTCAAAGCTTCTTACAAAAGAAACCTCTTTCACACCCTCCACGGGTCCCACCCACAGGCC 180
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1906 GTCAAAGCTTCTTACAAGAGAAACCTCTTTCACACCCTCCACGGGTCCCACCCACAGGCC 1965

Qy        181 ACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1966 ACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCA 2025

Qy        241 GCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2026 GCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACA 2085

Qy        301 TGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2086 TGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGG 2145

Qy        361 ACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2146 ACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGG 2205

Qy        421 GCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2206 GCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGC 2265

Qy        481 CCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2266 CCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGG 2325

Qy        541 CAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2326 CAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACA 2385

Qy        601 GCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2386 GCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAAC 2445

Qy        661 CCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2446 CCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAG 2505

Qy        721 TGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTA 780
              |||||||||||||||||  |||||||||||||||||||||||||||||||||||||||||
Db       2506 TGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTA 2565

Qy        781 AGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 AGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGC 2625

Qy        841 AACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 AACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGG 2685

Qy        901 AGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTAT 941
              ||||| ||| |  ||||  |  |  |     |  || | ||
Db       2686 AGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCAT 2726

RESULT 7
US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
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;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV
;  CURRENT APPLICATION NUMBER: US/09/964,469
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 36651
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(36651)
;   OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

  Query Match             39.5%;  Score 867.4;  DB 4;  Length 36651;
  Best Local Similarity   95.1%;  Pred. No. 1.8e-203;
  Matches  895;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          1 GACCCTAAGATGAAGGGACCTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTGCTTTC 60
              ||||||||||||||||||||         ||      |||| |      |||  ||||||
Db       1786 GACCCTAAGATGAAGGGACCAGTGGGGAGGTGGCCCCGGCAGGTGTCCCAGCAGCTTTC 1845

Qy         61 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGCAGTTCCTGGCGGGCTATACATAGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1846 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGCAGTTCCTGGCGGGCTATACATAGCCA 1905

Qy        121 GTCAAAGCTTCTTACAAAAGAAACCTCTTTCACACCCTCCACGGGTCCCACCCACAGGCC 180
              ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1906 GTCAAAGCTTCTTACAAGAGAAACCTCTTTCACACCCTCCACGGGTCCCACCCACAGGCC 1965

Qy        181 ACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1966 ACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCA 2025

Qy        241 GCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2026 GCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACA 2085

Qy        301 TGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2086 TGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGG 2145

Qy        361 ACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2146 ACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGG 2205

Qy        421 GCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2206 GCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGC 2265

Qy        481 CCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2266 CCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGG 2325

Qy        541 CAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2326 CAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACA 2385

Qy        601 GCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2386 GCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAAC 2445

Qy        661 CCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2446 CCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAG 2505

Qy        721 TGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTA 780
              |||||||||||||||||  |||||||||||||||||||||||||||||||||||||||||
Db       2506 TGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTA 2565

Qy        781 AGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2566 AGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGC 2625

Qy        841 AACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2626 AACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGG 2685

Qy        901 AGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTAT 941
              ||||| ||| |  ||||  |  |  |     |  || | ||
Db       2686 AGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCAT 2726

RESULT 8
US-08-464-954A-2
; Sequence 2, Application US/08464954A
; Patent No. 6255069
;  GENERAL INFORMATION:
;    APPLICANT:  BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI,
;    APPLICANT:  PRIYA
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR
;    TITLE OF INVENTION:  MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR
;    TITLE OF INVENTION:  KINASES GRK5 AND GRK6
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jane Massey Licata, Esq.
;      STREET:  Woodland Falls Corporate Park
;      STREET:  210 Lake Drive East, Suite 201
;      CITY:  Cherry Hill
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,954A
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076,084
;      FILING DATE:  June 11, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane Massey Licata
;      REGISTRATION NUMBER:  32,257
;      REFERENCE/DOCKET NUMBER:  JEFF-0118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (609) 779-2400
;      TELEFAX:  (609) 779-8488
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2848
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    ANTI-SENSE:  NO
US-08-464-954A-2

  Query Match             19.1%;  Score 419.8;  DB 3;  Length 2848;
  Best Local Similarity   56.2%;  Pred. No. 1.1e-93;
  Matches  891;  Conservative    0;  Mismatches  682;  Indels   12;  Gaps    5;

Qy        305 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 364
              ||  || || ||| |  | || ||||| |     ||  |||||||| |       |   |
Db         65 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGAAGGTGGCGGTGG 124
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Qy       365 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 421
               |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db       125 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 184

Qy       422 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 481
              ||||  ||||| || |  |  ||    |   |||  |||||||||||| |||| |||  |
Db       185 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACGC 244

Qy       482 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 541
             ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db       245 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 304

Qy       542 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 601
               ||||||| || |  |||    | |  ||  || ||  ||| |          || |   |
Db       305 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 364

Qy       602 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 661
              | || ||| |   |   |   | || |  |||   | | |  || |    |   |
Db       365 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 421

Qy       662 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 721
               ||| | | |||   ||| | | |  |  || ||| ||     | | |     || |
Db       422 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 480

Qy       722 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781
               ||            | |  ||||||  ||   |  | | ||   | |   || |||
Db       481 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 538

Qy       782 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 841
              || | | |   ||||  || || | ||   ||  ||||||||||     | || | |||
Db       539 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 598

Qy       842 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901
              |||||| |  | ||   ||||||   | | | |||| ||||| |||||||| ||||||||
Db       599 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 658

Qy       902 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 961
             ||| || |||  |||||||     ||| || ||||||||||||||| ||||| || || ||
Db       659 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 718

Qy       962 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 1021
              |||||| | ||||||      || |||   ||||| ||    || ||| | ||| ||||
Db       719 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 778

Qy      1022 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 1081
             ||| || | |||    ||  | ||     |||||||  || ||||| ||||  |   ||
Db       779 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTATGAGACCAAGGACGCGCT 838

Qy      1082 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 1141
              ||||| ||  |||  ||||||| ||||| |||||||||||||||||||||| || ||||
Db       839 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 898

Qy      1142 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 1201
             |  |  |||| |   |      ||||   |||| ||| | ||| ||||   ||||||  |
Db       899 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 958

Qy      1202 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 1261
             |  | |||| ||        ||||||| ||  ||||| ||||||| |||||  |  | ||
Db       959 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 1018

Qy      1262 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1321
             |||||||| |||| ||  | |  | ||||||||||| || ||| |  ||   |  ||
Db      1019 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1078

Qy      1322 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1381
             | || ||||||    | | |  || |||   |||||||||||||| |||    |  || |
Db      1079 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1135

Qy      1382 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1441
              || | | | ||  | |        |||||||  ||  | || |||  | | || || ||
Db      1136 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1195

Qy      1442 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1501
             | |  | || |   | || ||| |  |     ||| | ||| |||     |||||  || |
Db      1196 GATCACAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1255

Qy      1502 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1561
             ||          | | | |   |   | |      |        | | |  |||
Db      1256 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGGTTTTCCCCGCAGGCCCGCTC 1315

Qy      1562 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1621
             |  |   |    |||| |||      |     | || |  |      |  |  | |  |
Db      1316 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGCCTGGGGTGTCGTGGGGGCAG 1375

Qy      1622 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1681
               |    ||    | | | || |   |||||||| | | | |||||    || |||| |||
Db      1376 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1435

Qy      1682 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1741
             |||| |  | || || || ||   ||| ||||||    |   ||||   ||| ||  |
Db      1436 TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGTTCT 1495

Qy      1742 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1801
              || |||||  | ||||||  |||   ||| |||||  | ||    |  ||  |||||||
Db      1496 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGCAGTT 1555

Qy      1802 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1861
             || | | || ||||| |||||   ||| || ||  | |||||| | || ||  | || ||
Db      1556 CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1615

Qy      1862 GGGACTGTTTGAGGAACTGAATGAC 1886
              |     ||  | || ||||||| |
Db      1616 CGAGTGCTTCCAAGAGCTGAATGTC 1640


RESULT 9
US-08-221-817-12
; Sequence 12, Application US/08221817
; Patent No. 5532151
;  GENERAL INFORMATION:
;    APPLICANT:  Chantry, David
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Hoekstra, Merle F.
;    TITLE OF INVENTION:  A No. 5532151el G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,817
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/123,932
;      FILING DATE:  17 SEP 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5532151and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31981
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  12:
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;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2204 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  31..1758
US-08-221-817-12

  Query Match             19.0%;  Score 418.2;  DB 1;  Length 2204;
  Best Local Similarity   56.2%;  Pred. No. 2.5e-93;
  Matches  890;  Conservative    0;  Mismatches  683;  Indels   12;  Gaps    5;

Qy          305 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 364
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Db           33 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 92

Qy          365 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 421
                  |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db           93 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 152

Qy          422 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 481
                 ||||  ||||| || |  |  ||    |   |||  ||||||||||| |||| ||| |
Db          153 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACCG 212

Qy          482 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 541
                ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db          213 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 272

Qy          542 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 601
                  ||||||| || |  |||    | |  ||  || ||  ||| |        || |   |
Db          273 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 332

Qy          602 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 661
                 | || ||| |   |   |   | || |  |||   | | |  || |    |   |
Db          333 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 389

Qy          662 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 721
                  ||| | | |||   ||| | | |  |  || ||| ||     | | |     || |
Db          390 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 448

Qy          722 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781
                  ||            | |  ||||||  ||   |  | | ||   | |   || |||
Db          449 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 506

Qy          782 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 841
                 || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db          507 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 566

Qy          842 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901
                 |||||| |  | ||   |||||   | | | |||| ||||| |||||||| ||||||||
Db          567 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGTAAAGGTGGCTTTGGGGA 626

Qy          902 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 961
                ||| || |||  |||||||     ||| || |||||||||||||| ||||| || || ||
Db          627 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 686

Qy          962 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 1021
                 |||||| | ||||||      || |||   ||||| ||    || ||| | ||| ||||
Db          687 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 746

Qy         1022 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 1081
                ||| || | |||    ||  | ||     ||||||| |||| ||||| ||||  |   ||
Db          747 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTATGAGACCAAGGACGCGCT 806

Qy         1082 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 1141
                 ||||| ||  |||  |||||||| ||||| ||||||||||||||||||||| || ||||
Db          807 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 866

Qy         1142 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 1201
                |  |  |||| |   |      ||||   |||| ||| | ||| ||||   ||||||  |
Db          867 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 926

Qy         1202 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 1261
                |  | |||| ||        ||||||| ||  ||||| ||||||| |||||  |  | ||
Db          927 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 986

Qy         1262 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1321
                |||||||| |||| ||  | |  | ||||||||||| || || ||| |  ||   |  ||
Db          987 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1046

Qy         1322 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1381
                | || ||||||    | | |  || |||   |||||||||||||| |||    |  || |
Db         1047 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1103

Qy         1382 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1441
                 || | | | ||  | |        |||||||  ||  | || |||  | | || || ||
Db         1104 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1163

Qy         1442 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1501
                | | || || |   | || ||| |  |    ||| | ||| |||     |||||  || |
Db         1164 GATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1223

Qy         1502 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1561
                ||          | | | |   |   | |      |       | | |  |||
Db         1224 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGCTTTTCCCCGCAGGCCCGCTC 1283

Qy         1562 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1621
                |  |   |    |||| |||      |     | || |  |      |  |  | |  |
Db         1284 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGCCTGGGGTGTCGTGGGGGCAG 1343

Qy         1622 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1681
                  |    ||    | | | || |   ||||||| | | | |||||    || |||| |||
Db         1344 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1403

Qy         1682 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1741
                |||| |  | || || || ||   ||| |||||    |   ||||   ||| ||  |
Db         1404 TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGTTCT 1463

Qy         1742 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1801
                 || |||||  | ||||||  |||   ||| |||||  | ||    |  ||  || | ||
Db         1464 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGGACTT 1523

Qy         1802 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1861
                || | | || ||||| |||||   ||| || ||  | |||||| | || ||  | || ||
Db         1524 CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1583

Qy         1862 GGGACTGTTTGAGGAACTGAATGAC 1886
                 |     ||  | || ||||||| |
Db         1584 CGAGTGCTTCCAAGAGCTGAATGTC 1608


RESULT 10
US-08-454-439-12
; Sequence 12, Application US/08454439
; Patent No. 5591618
;  GENERAL INFORMATION:
;    APPLICANT:  Chantry, David
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Hoekstra, Merle F.
;    TITLE OF INVENTION:  A No. 5591618el G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/454,439
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,817
;      FILING DATE:  31-MAR-1994
;      APPLICATION NUMBER:  08/123,932
;      FILING DATE:  17 SEP 1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5591618and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31981
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2204 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  31..1758
US-08-454-439-12

  Query Match             19.0%;  Score 418.2;  DB 1;  Length 2204;
  Best Local Similarity   56.2%;  Pred. No. 2.5e-93;
  Matches  890;  Conservative    0;  Mismatches  683;  Indels   12;  Gaps    5;

Qy        305 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 364

Db         33 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 92

Qy        365 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 421

Db         93 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 152

Qy        422 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 481

Db        153 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACCG 212

Qy        482 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 541

Db        213 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 272

Qy        542 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 601

Db        273 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 332

Qy        602 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 661

Db        333 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 389

Qy        662 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 721

Db        390 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 448

Qy        722 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781

Db        449 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 506

Qy        782 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 841

Db        507 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 566

Qy        842 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901

Db        567 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGTAAAGGTGGCTTTGGGGA 626

Qy        902 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 961

Db        627 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 686

Qy        962 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 1021

Db        687 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 746

Qy       1022 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 1081

Db        747 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTATGAGACCAAGGACGCGCT 806

Qy       1082 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 1141

Db        807 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 866

Qy       1142 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 1201

Db        867 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 926

Qy       1202 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 1261

Db        927 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 986

Qy       1262 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1321

Db        987 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1046

Qy       1322 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1381

Db       1047 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1103

Qy       1382 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1441

Db       1104 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1163

Qy       1442 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1501

Db       1164 GATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1223

Qy       1502 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1561

Db       1224 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGCTTTTCCCCGCAGGCCCGCTC 1283

Qy       1562 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1621

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Qy       1622 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1681

Db       1344 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1403

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Qy       1742 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1801

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Qy       1802 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1861

Db       1524 CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1583

Qy       1862 GGGACTGTTTGAGGAACTGAATGAC 1886

Db       1584 CGAGTGCTTCCAAGAGCTGAATGTC 1608

RESULT 11
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PCT-US94-10487-12
; Sequence 12, Application PC/TUS9410487
;  GENERAL INFORMATION:
;    APPLICANT:  ICOS Corporation
;    TITLE OF INVENTION:  A Novel G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10487
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/221,817
;      FILING DATE:  31 MAR 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/123,932
;      FILING DATE:  17 SEP 1993
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Noland, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27866/31981
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2204 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  31..1758
PCT-US94-10487-12

  Query Match             19.0%;  Score 418.2;  DB 5;  Length 2204;
  Best Local Similarity   56.2%;  Pred. No. 2.5e-93;
  Matches  890;  Conservative    0;  Mismatches  683;  Indels   12;  Gaps    5;

Qy        305 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 364
              ||  || || ||| |  | || ||||| |     ||  |||||||| |       |   |
Db         33 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 92

Qy        365 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 421
                |  ||||||   |     ||    ||||||  |  ||     | ||      |
Db         93 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 152

Qy        422 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 481
               ||||  ||||| || |  |  ||    |   |||  ||||||||||| |||| ||| |
Db        153 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACCG 212

Qy        482 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 541
              ||| || ||||  || ||||| ||  |||  |||||   |||   | |  ||      |
Db        213 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 272

Qy        542 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 601
                ||||||| || |  |||    | |  ||  || ||  ||| |        || |   |
Db        273 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 332

Qy        602 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 661
               | || ||| |   |   |   | || |  |||   | | |  || |    |   |
Db        333 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 389

Qy        662 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 721
                ||| | | |||   ||| | | |  |  || ||| ||     | | |     || |
Db        390 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 448

Qy        722 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781
                ||            | |  ||||||  ||   |  | | ||   | |   || |||
Db        449 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 506

Qy        782 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 841
               || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db        507 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 566

Qy        842 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901
               |||||| |  | ||   |||||   | | | |||| ||||| |||||||| ||||||||
Db        567 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGTAAAGGTGGCTTTGGGGA 626

Qy        902 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 961
              ||| || |||  |||||||     ||| || |||||||||||||| ||||| || || ||
Db        627 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 686

Qy        962 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 1021
               |||||| | ||||||      || |||   ||||| ||    || ||| | ||| ||||
Db        687 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 746

Qy       1022 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 1081
              ||| || | |||    ||  | ||     ||||||| |||| ||||| ||||  |   ||
Db        747 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTATGAGACCAAGGACGCGCT 806

Qy       1082 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 1141
               ||||| ||  |||  |||||||| ||||| ||||||||||||||||||||| || ||||
Db        807 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 866

Qy       1142 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 1201
              |  |  |||| |   |      ||||   |||| ||| | ||| ||||   ||||||  |
Db        867 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 926

Qy       1202 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 1261
              |  | |||| ||        ||||||| ||  ||||| ||||||| |||||  |  | ||
Db        927 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 986

Qy       1262 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1321
              |||||||| |||| ||  | |  | ||||||||||| || || ||| |  ||   |  ||
Db        987 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1046

Qy       1322 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1381
              | || ||||||    | | |  || |||   |||||||||||||| |||    |  || |
Db       1047 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1103

Qy       1382 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1441
               || | | | ||  | |        |||||||  ||  | || |||  | | || || ||
Db       1104 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1163

Qy       1442 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1501
              | | || || |   | || ||| |  |    ||| | ||| |||     |||||  || |
Db       1164 GATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1223

Qy       1502 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1561
              ||          | | | |   |   | |      |       | | |  |||
Db       1224 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGCTTTTCCCCGCAGGCCCGCTC 1283

Qy       1562 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1621
              |  |   |    |||| |||      |     | || |  |      |  |  | |  |
Db       1284 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGCCTGGGGTGTCGTGGGGGCAG 1343

Qy       1622 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1681
                |    ||    | | | || |   ||||||| | | | |||||    || |||| |||
Db        1344 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1403

Qy        1682 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1741
               |||| |  | || || || ||   ||| |||||    |   ||||   ||| ||  |
Db        1404 TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGTTCT 1463

Qy        1742 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1801
                || |||||  | ||||||  |||   ||| |||||  | ||    |  ||  || | ||
Db        1464 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGGACTT 1523

Qy        1802 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1861
               || | | || ||||| |||||   ||| || ||  | |||||| | || ||  | || ||
Db        1524 CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1583

Qy        1862 GGGACTGTTTGAGGAACTGAATGAC 1886
                |     ||  | || ||||||| |
Db        1584 CGAGTGCTTCCAAGAGCTGAATGTC 1608


RESULT 12
US-08-221-817-21
; Sequence 21, Application US/08221817
; Patent No. 5532151
;  GENERAL INFORMATION:
;    APPLICANT:  Chantry, David
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Hoekstra, Merle F.
;    TITLE OF INVENTION:  A No. 5532151el G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,817
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/123,932
;      FILING DATE:  17 SEP 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5532151and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31981
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1983 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  13..1740
US-08-221-817-21

  Query Match             18.0%;  Score 395.8;  DB 1;  Length 1983;
  Best Local Similarity   55.3%;  Pred. No. 7.9e-88;
  Matches  876;  Conservative    0;  Mismatches  697;  Indels   12;  Gaps    5;
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Qy         305 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 364
               ||  || || ||| |  | || ||||| |     ||  ||||||||| |       | | |
Db          15 GGAGCTCGAGAACATCGTAGCGAACACGGGGCTACTCAAGGCCCGGGAAGGTGGTGGCGG 74

Qy         365 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 421
                 |  | ||||   ||    ||    |||| |  |  |||    | |||    |
Db          75 GAATCGTAAAGGCAAGAGCAAGAAATGGCGCCAGATGCTGCAGTTCCCCCACATCAGCCA 134

Qy         422 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 481
                || |  |||||||| |  |   ||   |   ||| |||||||||||||||||  ||| |
Db         135 GTGTGAAGAGCTCCGGCTCACCTTGGAACGTGACTACCACAGCCTGTGTGAGCGTCAGTC 194

Qy         482 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 541
               ||| || ||||   | ||  |||| |||   || ||   |||   | |   |       |
Db         195 CATTGGGCGCCTGTTATTATGTGAGTTCTGCGCTACGAGGCCTGAGCTGACCCGCTGTAC 254

Qy         542 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 601
                 ||||||| || |  |||    | |  ||| || ||   || |        || |   |
Db         255 TGCCTTCCTGGATGGGGTGGCTGAGTATGAGGTGACCCCTGATGAGAAACGGAAGGCATG 314

Qy         602 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 661
                | ||  |   ||||  ||   | || |  |||   | | |  || |    |   |
Db         315 TGGGCGTC---GGCTAATGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 371

Qy         662 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 721
                 | | | | |||   |||   | |  ||||| ||| || |   | | |     || |
Db         372 AGTTCCCCGGCAGCTGGTGAGTAAC-TGTGCCCAGCGGCTAGAGCAGGGACCCTGCAAAG 430

Qy         722 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781
                 ||              |  ||||||  |    |       ||| | ||  || |||
Db         431 ACCTCTTCCAGGAGCTGACCCGGCTGACCCATGAGTACCTAAGCATGGGC--CCTTTTGG 488

Qy         782 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 841
                || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db         489 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 548

Qy         842 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901
                |||||| |  | ||   ||| |   ||| | |||| ||||| |||||||| ||||||||
Db         549 GCCAGTGACCAAAAACACCTTTAGGCAGTACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 608

Qy         902 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 961
               ||| ||||||  |||||||   |  || || ||||||||||| |  || ||   | | ||
Db         609 GGTGTGTGCCTGCCAGGTGCGGACAACAGGCAAGATGTATGCGTACAAAAACTGGAAAAA 668

Qy         962 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 1021
               ||| ||  | ||||||      || |||   ||| |||||   || ||| | ||| ||||
Db         669 GAAACGAATAAAGAAGCGGAAGGGGGAGGCCATGTCTCTCAACGAGAAGCAGATCCTGGA 728

Qy        1022 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 1081
               ||| || | |||    ||  | ||     | ||||| || | ||||| ||||      ||
Db         729 GAAAGTGAACAGTAGGTTTGTAGTGATCTTAGCCTACGCATATGAGACCAAGGATGCACT 788

Qy        1082 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 1141
                ||||| ||  |||   |||||||||| || ||||||||||||||||||||| || ||||
Db         789 GTGCCTGGTGCTGACATTGATGAATGGAGGCGACCTCAAGTTCCACATCTACCACATGGG 848

Qy        1142 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 1201
               |  |  |||| |   |      || |   | || ||  | ||| ||||   ||||||  |
Db         849 CCAGGCTGGCTTTCCCGAAGCACGTGCTGTGTTCTATGCTGCCGAGATCTGCTGTGGTCT 908

Qy        1202 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 1261
               |  | || | ||        ||||||| ||  ||||| | ||||| ||||||| | |||||
Db         909 GGAGGACTTACACCGGGAACGCATCGTGTACAGGGACCTAAAGCCAGAGAATATCCTTCT 968

Qy        1262 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1321
               ||||||||  ||| ||    |  | || ||||||||| ||||| ||| |  |    |  ||
Db         969 GGATGACCATGGCCACATTCGAATCTCCGACCTGGGCCTGGCTGTGCATGTTCCTGAGGG 1028

Qy        1322 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1381
               | || |||||||      | |  || ||    || ||||||||||| |||    |  || |
Db        1029 CCAGACCATCAAAGGCCGTGTGGGCACTGTGGGCTACATGGCTCCAGAG---GTGGTGAA 1085
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Qy       1382 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1441
               || |   | ||  | |    |   |||||||  ||  | || |||  | | || || ||
Db       1086 GAATGAGCGCTACACATTCAGTCCTGACTGGTGGGCGCTAGGCTGCCTCCTGTACGAGAT 1145

Qy       1442 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1501
              | |||| ||||   | || ||| |  |    ||| | ||| |||     |||||  || |
Db       1146 GATTGCGGGACAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1205

Qy       1502 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1561
              ||          | | |  |  |   | | |    |      || | || ||| |
Db       1206 GCGGCTGGTCAAGGAGGTGGCTGAGGAGTACACCGACCGCTTCTCCCCACAGGCACGCTC 1265

Qy       1562 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1621
              |     ||    |||  ||       |     | ||||  |      |  |  |||
Db       1266 ACTCTGTTCTCAGCTTCTCAACAAGGACCCTGCTGAGCGCCTGGGGTGTCGTGGAGGTGG 1325

Qy       1622 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1681
                |   |||    | | | || |   | || || |   | || ||    || |||| |||
Db       1326 TGCCCGTGAGGTAAAGGAGCACCCCCTTTTCAAGAAACTGAATTTCAAGCGGCTGGGAGC 1385

Qy       1682 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1741
              |||  |  | ||||| || |||   || |||||    |   ||||   ||| ||| |
Db       1386 TGGAATGCTAGAACCACCTTTTAAACCTGACCCCCAGGCCATTTACTGCAAGGACGTGCT 1445

Qy       1742 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1801
               || |||||  | |||||    |||   || |||||  | ||   || |||  |  | ||
Db       1446 GGACATTGAACAGTTCTCCACAGTTAAAGGTGTGGATCTGGAGCCCACAGACCAAGACTT 1505

Qy       1802 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1861
              || | | || ||||| || |||  |||  | ||  | |||||| | || ||  | || ||
Db       1506 CTACCAGAAGTTTGCCACGGGTAGTGTGTCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1565

Qy       1862 GGGACTGTTTGAGGAACTGAATGAC 1886
               |     ||  ||||||| |||| |
Db       1566 TGAGTGCTTCCAGGAACTAAATGTC 1590
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RESULT 13
US-08-454-439-21
; Sequence 21, Application US/08454439
; Patent No. 5591618
;  GENERAL INFORMATION:
;    APPLICANT:  Chantry, David
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Hoekstra, Merle F.
;    TITLE OF INVENTION:  A No. 5591618el G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/454,439
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,817
;      FILING DATE:  31-MAR-1994
;      APPLICATION NUMBER:  08/123,932
;      FILING DATE:  17 SEP 1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5591618and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31981
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1983 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  13..1740
US-08-454-439-21

  Query Match             18.0%;  Score 395.8;  DB 1;  Length 1983;
  Best Local Similarity   55.3%;  Pred. No. 7.9e-88;
  Matches  876;  Conservative    0;  Mismatches  697;  Indels   12;  Gaps    5;

Qy        305 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 364
              ||  || || ||| |  | || ||||| |     ||  |||||||| |       | | |
Db         15 GGAGCTCGAGAACATCGTAGCGAACACGGGGCTACTCAAGGCCCGGGAAGGTGGTGGCGG 74

Qy        365 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 421
                |  | ||||   ||    ||    |||| |  |  |||    | |||    |
Db         75 GAATCGTAAAGGCAAGAGCAAGAAATGGCGCCAGATGCTGCAGTTCCCCCACATCAGCCA 134

Qy        422 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 481
               || |  |||||||| |  |   ||   |   ||| ||||||||||||||||||  ||| |
Db        135 GTGTGAAGAGCTCCGGCTCACCTTGGAACGTGACTACCACAGCCTGTGTGAGCGTCAGTC 194

Qy        482 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 541
              ||| || ||||   | ||  |||| |||   || ||   |||   | |   |       |
Db        195 CATTGGGCGCCTGTTATTATGTGAGTTCTGCGCTACGAGGCCTGAGCTGACCCGCTGTAC 254

Qy        542 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 601
                ||||||| || |  |||    | |  ||| || ||   || |        || |   |
Db        255 TGCCTTCCTGGATGGGGTGGCTGAGTATGAGGTGACCCCTGATGAGAAACGGAAGGCATG 314

Qy        602 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 661
               | ||  |   ||||  ||   | || |  |||   | | |  || |    |   |
Db        315 TGGGCGTC---GGCTAATGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 371

Qy        662 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 721
                | | | | |||   |||   | |  ||||| ||| || |   | | |     || |
Db        372 AGTTCCCCGGCAGCTGGTGAGTAAC-TGTGCCCAGCGGCTAGAGCAGGGACCCTGCAAAG 430

Qy        722 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781
                ||              |  ||||||  |    |       ||| | ||  || |||
Db        431 ACCTCTTCCAGGAGCTGACCCGGCTGACCCATGAGTACCTAAGCATGGGC--CCTTTTGG 488

Qy        782 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 841
               || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db        489 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 548

Qy        842 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901
               |||||| |  | ||   ||| |   ||| | |||| ||||| ||||||||| ||||||||
Db        549 GCCAGTGACCAAAAACACCTTTAGGCAGTACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 608

Qy        902 GGTATGTGCCGTCCAGGTGAAAAACACTGGAAAGATGTATGCCTGTAAGAAACTGGACAA 961
              ||| ||||||  |||||||   |  || || ||||||||||| |  || ||   | | ||
Db        609 GGTGTGTGCCTGCCAGGTGCGGACAACAGGCAAGATGTATGCGTACAAAAACTGGAAAAA 668

Qy        962 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 1021
              ||| ||  | ||||||      || |||   ||| |||||   || ||| | ||| ||||
Db        669 GAAACGAATAAAGAAGCGGAAGGGGGAGGCCATGTCTCTCAACGAGAAGCAGATCCTGGA 728

Qy       1022 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 1081
              ||| || | |||    ||  | ||     | ||||| || | ||||| ||||      ||
Db        729 GAAAGTGAACAGTAGGTTTGTAGTGATCTTAGCCTACGCATATGAGACCAAGGATGCACT 788
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Qy       1082 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 1141
               ||||| ||  |||   |||||||||| || ||||||||||||||||||||| || ||||
Db        789 GTGCCTGGTGCTGACATTGATGAATGGAGGCGACCTCAAGTTCCACATCTACCACATGGG 848

Qy       1142 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 1201
              |  |  |||| |   |      || |   | || ||  | ||| ||||   ||||||  |
Db        849 CCAGGCTGGCTTTCCCGAAGCACGTGCTGTGTTCTATGCTGCCGAGATCTGCTGTGGTCT 908

Qy       1202 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 1261
              |  | || | ||        ||||||| ||  ||||| | ||||| |||||| | |||||
Db        909 GGAGGACTTACACCGGGAACGCATCGTGTACAGGGACCTAAAGCCAGAGAATATCCTTCT 968

Qy       1262 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1321
              ||||||||  ||| ||    |  | ||  ||||||||  ||||| ||| |  |    |  ||
Db        969 GGATGACCATGGCCACATTCGAATCTCCGACCTGGGCCTGGCTGTGCATGTTCCTGAGGG 1028

Qy       1322 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1381
              | || ||||||      | |  || ||    || ||||||||||| |||    |  || |
Db       1029 CCAGACCATCAAAGGCCGTGTGGGCACTGTGGGCTACATGGCTCCAGAG---GTGGTGAA 1085

Qy       1382 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1441
               || |   | ||  | |    |   |||||||  ||  | || |||  | | || || ||
Db       1086 GAATGAGCGCTACACATTCAGTCCTGACTGGTGGGCGCTAGGCTGCCTCCTGTACGAGAT 1145

Qy       1442 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1501
              | |||| ||||   | || ||| |  |    ||| | ||| |||     |||||  || |
Db       1146 GATTGCGGGACAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1205

Qy       1502 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1561
              ||          | | |  |  |   | | |    |      || | || ||| |
Db       1206 GCGGCTGGTCAAGGAGGTGGCTGAGGAGTACACCGACCGCTTCTCCCCACAGGCACGCTC 1265

Qy       1562 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1621
              |     ||    |||  ||       |     | ||||  |      |  |  |||
Db       1266 ACTCTGTTCTCAGCTTCTCAACAAGGACCCTGCTGAGCGCCTGGGGTGTCGTGGAGGTGG 1325

Qy       1622 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1681
                |   |||    | | | || |   | || || |   | || ||    || |||| |||
Db       1326 TGCCCGTGAGGTAAAGGAGCACCCCCTTTTCAAGAAACTGAATTTCAAGCGGCTGGGAGC 1385

Qy       1682 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1741
              |||  |  | ||||| || |||   || |||||    |   ||||   ||| ||| |
Db       1386 TGGAATGCTAGAACCACCTTTTAAACCTGACCCCCAGGCCATTTACTGCAAGGACGTGCT 1445

Qy       1742 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1801
               || |||||  | |||||    |||   || |||||  | ||   || |||  |  | ||
Db       1446 GGACATTGAACAGTTCTCCACAGTTAAAGGTGTGGATCTGGAGCCCACAGACCAAGACTT 1505

Qy       1802 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1861
              || | | || ||||| || |||  |||  | ||  | |||||| | || ||  | || ||
Db       1506 CTACCAGAAGTTTGCCACGGGTAGTGTGTCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1565

Qy       1862 GGACTGTTTTGAGGAACTGAATGAC 1886
               |     ||  ||||||| |||| |
Db       1566 TGAGTGCTTCCAGGAACTAAATGTC 1590


RESULT 14
PCT-US94-10487-21
; Sequence 21, Application PC/TUS9410487
;  GENERAL INFORMATION:
;    APPLICANT:  ICOS Corporation
;    TITLE OF INVENTION:  A Novel G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10487
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/221,817
;      FILING DATE:  31 MAR 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/123,932
;      FILING DATE:  17 SEP 1993
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Noland, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27866/31981
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1983 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  13..1740
PCT-US94-10487-21

  Query Match             18.0%;  Score 395.8;  DB 5;  Length 1983;
  Best Local Similarity   55.3%;  Pred. No. 7.9e-88;
  Matches  876;  Conservative    0;  Mismatches  697;  Indels   12;  Gaps    5;

Qy        305 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 364
              ||  || || ||| |  | || ||||| |     ||  |||||||| |       | | |
Db         15 GGAGCTCGAGAACATCGTAGCGAACACGGGGCTACTCAAGGCCCGGGAAGGTGGTGGCGG 74

Qy        365 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 421
                |  | ||||   ||    ||    |||| |  |  |||    | |||    |
Db         75 GAATCGTAAAGGCAAGAGCAAGAAATGGCGCCAGATGCTGCAGTTCCCCCACATCAGCCA 134

Qy        422 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 481
               || |  |||||||| |  |   ||   |   ||| |||||||||||||||||  ||| |
Db        135 GTGTGAAGAGCTCCGGCTCACCTTGGAACGTGACTACCACAGCCTGTGTGAGCGTCAGTC 194

Qy        482 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 541
              ||| || ||||   | ||  |||| |||   || ||   |||   | |   |       |
Db        195 CATTGGGCGCCTGTTATTATGTGAGTTCTGCGCTACGAGGCCTGAGCTGACCCGCTGTAC 254

Qy        542 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 601
                ||||||| || |  |||    | |  ||| || ||   || |        || |   |
Db        255 TGCCTTCCTGGATGGGGTGGCTGAGTATGAGGTGACCCCTGATGAGAAACGGAAGGCATG 314

Qy        602 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 661
               | ||  |   ||||  ||   | || |  |||   | | |  || |    |   |
Db        315 TGGGCGTC---GGCTAATGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 371

Qy        662 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 721
                | | | | |||   |||   | |  ||||| ||| || |   | | |     || |
Db        372 AGTTCCCCGGCAGCTGGTGAGTAAC-TGTGCCCAGCGGCTAGAGCAGGGACCCTGCAAAG 430

Qy        722 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781
                ||              |  ||||||  |    |       ||| | ||  || |||
Db        431 ACCTCTTCCAGGAGCTGACCCGGCTGACCCATGAGTACCTAAGCATGGGC--CCTTTTGG 488
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Qy       782 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 841
              || | | |   ||||  ||  || | ||   || ||||||||||||     | || | |||
Db       489 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 548

Qy       842 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901
              |||||| |  | ||   ||| |   ||| | |||| |||| |||||||| ||||||||
Db       549 GCCAGTGACCAAAAACACCTTTAGGCAGTACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 608

Qy       902 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 961
             ||| ||||||  |||||||   |  || || ||||||||||| |   | ||   | | ||
Db       609 GGTGTGTGCCTGCCAGGTGCGGACAACAGGCAAGATGTATGCGTACAAAAACTGGAAAAA 668

Qy       962 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 1021
             ||| ||  | ||||||      || |||   ||| |||||   || |||  | ||| ||||
Db       669 GAAACGAATAAAGAAGCGGAAGGGGGAGGCCATGTCTCTCAACGAGAAGCAGATCCTGGA 728

Qy      1022 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 1081
             ||| || | |||    ||  | ||     | ||||| || | ||||| ||||      ||
Db       729 GAAAGTGAACAGTAGGTTTGTAGTGATCTTAGCCTACGCATATGAGACCAAGGATGCACT 788

Qy      1082 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 1141
              ||||| ||  |||   ||||||||||| || |||||||||||||||||||||| || ||||
Db       789 GTGCCTGGTGCTGACATTGATGAATGGAGGCGACCTCAAGTTCCACATCTACCACATGGG 848

Qy      1142 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 1201
             |  |  |||| |   |       || |   | || ||  | ||| ||||   ||||||  |
Db       849 CCAGGCTGGCTTTCCCGAAGCACGTGCTGTGTTCTATGCTGCCGAGATCTGCTGTGGTCT 908

Qy      1202 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 1261
             |  | || | ||        ||||||| ||  ||||| | ||||| ||||||   |||||
Db       909 GGAGGACTTACACCGGGAACGCATCGTGTACAGGGACCTAAAGCCAGAGAATATCCTTCT 968

Qy      1262 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1321
             ||||||||  ||| ||    |  | || |||||||| |||| ||| ||  |    |    ||
Db       969 GGATGACCATGGCCACATTCGAATCTCCGACCTGGGCCTGGCTGTGCATGTTCCTGAGGG 1028

Qy      1322 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1381
             | || |||||||      | |  || ||    || |||||||||||| |||    |  || |
Db      1029 CCAGACCATCAAAGGCCGTGTGGGCACTGTGGGCTACATGGCTCCAGAG---GTGGTGAA 1085

Qy      1382 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1441
              || |   | ||  | |    |   |||||||  ||  |  || |||  | | || || ||
Db      1086 GAATGAGCGCTACACATTCAGTCCTGACTGGTGGGCGCTAGGCTGCCTCCTGTACGAGAT 1145

Qy      1442 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1501
             | |||| ||||   | || ||| |  |    ||| | ||| |||     |||||  || |
Db      1146 GATTGCGGGACAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1205

Qy      1502 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1561
             ||          | | |  |  |   | | |    |      || | || ||| |
Db      1206 GCGGCTGGTCAAGGAGGTGGCTGAGGAGTACACCGACCGCTTCTCCCCACAGGCACGCTC 1265

Qy      1562 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1621
             |     ||    |||  ||       |     | ||||  |      |  |  |||
Db      1266 ACTCTGTTCTCAGCTTCTCAACAAGGACCCTGCTGAGCGCCTGGGGTGTCGTGGAGGTGG 1325

Qy      1622 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1681
               |   |||    | | | || |   | || || |   | || ||    || |||| |||
Db      1326 TGCCCGTGAGGTAAAGGAGCACCCCCTTTTCAAGAAACTGAATTTCAAGCGGCTGGGAGC 1385

Qy      1682 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1741
             |||  |  | ||||| || |||    | ||||||    |    ||||   ||| ||| |
Db      1386 TGGAATGCTAGAACCACCTTTTAAACCTGACCCCCAGGCCATTTACTGCAAGGACGTGCT 1445

Qy      1742 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1801
              || |||||  | |||||    |||   || ||||||  | ||   || ||||  |  | ||
Db      1446 GGACATTGAACAGTTCTCCACAGTTAAAGGTGTGGATCTGGAGCCCACAGACCAAGACTT 1505

Qy      1802 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1861
             || | | || ||||| || |||  |||  | ||  | |||||| | || ||  | || ||
Db      1506 CTACCAGAAGTTTGCCACGGGTAGTGTGTCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1565

Qy      1862 GGGACTGTTTGAGGAACTGAATGAC 1886
              |     ||  ||||||| |||| |
Db      1566 TGAGTGCTTCCAGGAACTAAATGTC 1590

RESULT 15
US-08-221-817-10
; Sequence 10, Application US/08221817
; Patent No. 5532151
;  GENERAL INFORMATION:
;    APPLICANT:  Chantry, David
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Hoekstra, Merle F.
;    TITLE OF INVENTION:  A No. 5532151el G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,817
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/123,932
;      FILING DATE:  17 SEP 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5532151and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31981
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2206 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  31..1926
US-08-221-817-10

  Query Match             17.7%;  Score 389.4;  DB 1;  Length 2206;
  Best Local Similarity   55.3%;  Pred. No. 3.1e-86;
  Matches  866;  Conservative    0;  Mismatches  681;  Indels   18;  Gaps    5;

Qy       305 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 364
             ||  || || ||| |  | || ||||| |     ||  ||||||||| |      |   |
Db        33 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 92

Qy       365 CGACAGCAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 421
               |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db        93 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 152

Qy       422 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 481
              ||||  ||||| || |  |  ||    |   |||  ||||||||||| |||| ||| |
Db       153 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACCG 212

Qy       482 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 541
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              ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db       213 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 272

Qy       542 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 601
               ||||||| || |  |||    | |  ||  || ||  ||| |        || |   |
Db       273 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 332

Qy       602 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 661
              | || ||| |   |   |   | || |  |||   | | |  || |    |   |
Db       333 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 389

Qy       662 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 721
               ||| | | |||   ||| |   |     |||             ||| | |  |  |
Db       390 GGTCCCCCGGCAGCTGGTGACGGACTGCACCCAGCG------GCTGGAGCAGGGTCCTGC 443

Qy       722 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 781
                  |  |  |   |  | |  | |  | |       |     |       ||||||
Db       444 AAAGACCTTTTCCAGGAACTACCCGGCTGACCCACGAGTACCTGAGCGTGGCCCCTTTGC 503

Qy       782 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 841
              || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db       504 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 563

Qy       842 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 901
              |||||| |  | ||   |||||   | | | |||| ||||| |||||||| ||||||||
Db       564 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGTAAAGGTGGCTTTGGGGA 623

Qy       902 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 961
             ||| || |||  |||||||     ||| || |||||||||||||| ||||| || || ||
Db       624 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 683

Qy       962 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 1021
              |||||| | ||||||      || |||   ||||| ||    || ||| | ||| ||||
Db       684 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 743

Qy      1022 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 1081
             ||| || | |||    ||  | ||     | | ||| |||| ||||| ||||  |   ||
Db       744 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTCGGCTACGCCTATGAGACCAAGGACGCGCT 803

Qy      1082 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 1141
              ||||| ||  |||  |||||||| ||||| ||||||||||||||||||||| || ||||
Db       804 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 863

Qy      1142 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 1201
             |  |  |||| |   |      ||||   |||| ||| | ||| ||||   ||||||  |
Db       864 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 923

Qy      1202 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 1261
             |  | |||| ||        ||||||| ||  ||||| ||||||| |||||  |  | ||
Db       924 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 983

Qy      1262 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1321
             |||||||| |||| ||  | |  | ||||||||||| || || ||| |  ||   |  ||
Db       984 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1043

Qy      1322 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1381
             | || ||||||    | | |  || |||   |||||||||||||| |||    |  || |
Db      1044 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1100

Qy      1382 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1441
              || | | | ||  | |        |||||||  ||  | || |||  | | || || ||
Db      1101 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1160

Qy      1442 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1501
             | | || || |   | || ||| |  |    ||| | ||| |||     |||||  || |
Db      1161 GATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1220

Qy      1502 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1561
             ||          | | | |   |   | |      |       | | |  |||
Db      1221 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGCTTTTCCCCGCAGGCCCGCTC 1280

Qy      1562 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1621
             |  |   |    |||| |||      |     | || |    | | ||  |  | |
Db      1281 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACCGACCCTGGGGTGTCGTGGGGG 1340

Qy      1622 GTCTG---ATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGA 1678
                ||     ||    | | | || |   ||||||| | | | |||||    || ||||
Db      1341 CAGTGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGG 1400

Qy      1679 AGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACAT 1738
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Db      1401 AGCTGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGT 1460

Qy      1739 CGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCA 1798
                 || |||||  | ||||||  |||   ||| |||||  | ||    |  ||  || |
Db      1461 TCTGGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGGA 1520

Qy      1799 GTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGA 1858
              |||| | | || ||||| |||||   ||| || ||  | |||||| | || ||  | ||
Db      1521 CTTCTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGA 1580

Qy      1859 AACGG 1863
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Db      1581 GACCG 1585
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Search completed: August 13, 2004, 18:45:32
Job time : 121.544 secs

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                    GenCore version 5.1.6
             Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          August 13, 2004, 06:21:35 ; Search time 589.249 Seconds
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Title:           US-10-044-205A-1
Perfect score:   2198
Sequence:        1 gaccctaagatgaagggacc..........aacactcaggtttattttga 2198

Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters:      6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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     Pred. No. is the number of results predicted by chance to have a
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     1     2198   100.0   2198  7  ABS57375                          Abs57375 cDNA enco
     2   2008.8    91.4   2249  4  AAH78799                          Aah78799 Human G-p
     3   1988.8    90.5   3186  7  ACC44827                          Acc44827 Human G p
     4   1817.8    82.7   1821  9  ADC39221                          Adc39221 Novel hum
     5   1757.8    80.0   1761  7  ABZ56943                          Abz56943 Human gen
     6   1658.8    75.5   1662  6  ABQ86178                          Abq86178 Novel hum
     7   1658.8    75.5   1662  6  AAD26466                          Aad26466 Human kin
     8   1658.8    75.5   1662  6  AAD46350                          Aad46350 Human con
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    10   1657.2    75.4   1662  6  AAD28071                          Aad28071 Human kin
    11   1655.6    75.3   1662  4  AAS06702                          Aas06702 Polynucle
    12   1655.6    75.3   1662  7  ACC44826                          Acc44826 Human G p
    13   1187.8    54.0   1191  7  ABZ56934                          Abz56934 Human RGS
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    17    419.8    19.1   2848  4  AAH24842                          Aah24842 Nucleotid
    18    418.2    19.0   2204  2  AAQ87426                          Aaq87426 Human GRK
    19    418.2    19.0   2848  6  ABL61805                          Abl61805 Colon ade
    20    418.2    19.0   2848  6  ABK49405                          Abk49405 cDNA enco
    21    403.8    18.4   2541  9  ADB53307                          Adb53307 Primary r
    22    395.8    18.0   1983  2  AAQ87427                          Aaq87427 Rat GRK c
    23    389.4    17.7   2206  2  AAQ87425                          Aaq87425 Human GRK
    24    377.8    17.2   2519  7  ACA03892                          Aca03892 cDNA upre
    25    374.6    17.0   2519  9  ADB47372                          Adb47372 Human cDN
    26      373    17.0   2511  2  AAV71032                          Aav71032 Grk5-gree
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    31    368.2    16.8   2557  6  ABK49404                          Abk49404 cDNA enco
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    34    320.6    14.6   2017  2  AAX90219                          Aax90219 GRK4 poly
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    36    311.6    14.2   1879  2  AAX90221                          Aax90221 GRK4 poly
    37    311.6    14.2   1886  2  AAQ75116                          Aaq75116 Composite
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    39    262.4    11.9   2947  5  AAS86360                          Aas86360 DNA encod
    40    253.2    11.5   1324  2  AAX90223                          Aax90223 GRK4 poly
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    42    158.4     7.2    493  8  ACH50623                          Ach50623 Human mam
    43    153.4     7.0   3154  8  ACD44895                          Acd44895 Human sig
    44      151     6.9   2037  6  ABT06290                          Abt06290 Human NOV
    45      151     6.9   2067  6  AAK99675                          Aak99675 2067nt hu

                                  ALIGNMENTS

RESULT 1
ABS57375
ID   ABS57375 standard; cDNA; 2198 BP.
XX
AC   ABS57375;
XX
DT   04-FEB-2003  (first entry)
XX
DE   cDNA encoding human GPCR kinase (GPCRK) 69087.
XX
KW   Human; G protein coupled receptor kinase; GPCRK 69087;
KW   cellular proliferative disorder; differentiative disorder;
KW   haematopoietic neoplastic disorder; leukaemia; carcinoma; sarcoma;
KW   metastatic disorder; cytostatic; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             291. .1952
FT                   /*tag=  a
FT                   /product= "GPCRK 69087"
FT                   /note= "The coding sequence given as SEQ ID No:3 is
FT                   specifically claimed in Claim 1"
XX
PN   US2002123464-A1.
XX
PD   05-SEP-2002.
XX
PF   22-OCT-2001; 2001US-00044205.
XX
PR   19-OCT-2000; 2000US-0241884P.
PR   20-OCT-2000; 2000US-0241877P.
PR   23-OCT-2000; 2000US-0242428P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R,  Bandaru R;
XX
DR   WPI; 2003-066811/06.
DR   P-PSDB; ABG72173.
XX
PT   Novel isolated G protein coupled receptor kinase, 69087, nuclear
PT   signaling protein, 15821 or mitogen activated protein kinase phosphatase,
PT   15418, useful for treating cellular proliferative or differentiative
PT   disorders.
XX
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PS   Claim 1; Fig 1; 98pp; English.
XX
CC   The present invention relates to the isolation of a novel human G protein
CC   coupled receptor (GPCR) kinase (GPCRK) designated 69087), a novel human
CC   nuclear signalling protein designated 15821, and a novel human mitogen-
CC   activated protein kinase (MAPK) phosphatase MAPKP designated 15418, and
CC   the polynucleotide sequences encoding them. The sequences of the
CC   invention are useful for treating and diagnosing disorders such as
CC   cellular proliferative and differentiative disorders (e.g. haematopoietic
CC   neoplastic disorders, leukaemia, carcinoma, sarcoma or metastatic
CC   disorders). They are also useful in screening assays, detection assays
CC   (e.g. chromosomal mapping, tissue typing, forensic biology), predictive
CC   medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical
CC   trials and pharmacogenomics), and in methods of treatment (e.g.
CC   therapeutic and prophylactic). The sequences may also be used to screen
CC   public databases to identify other family members or related sequences.
CC   The polypeptide sequences are useful as immunogens to generate antibodies
CC   that bind the polypeptides. The polynucleotide sequences are useful for
CC   mapping their respective genes on a chromosome, identifying gene regions
CC   associated with cellular proliferative or differentiative disorders, and
CC   in gene therapy. The present sequence encodes human GPCRK 69087
XX
SQ   Sequence 2198 BP; 558 A; 557 C; 607 G; 476 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 2198;  DB 7;  Length 2198;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 2198;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GACCCTAAGATGAAGGGACCTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTGCTTTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACCCTAAGATGAAGGGACCTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTGCTTTC 60

Qy         61 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGCAGTTCCTGGCGGGCTATACATAGCCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GCCTTGGCAGGTGGGAGCATGACCTATCGTGTGCAGTTCCTGGCGGGCTATACATAGCCA 120

Qy        121 GTCAAAGCTTCTTACAAAAGAAACCTCTTTCACACCCTCCACGGGTCCCACCCACAGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTCAAAGCTTCTTACAAAAGAAACCTCTTTCACACCCTCCACGGGTCCCACCCACAGGCC 180

Qy        181 ACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCA 240

Qy        241 GCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 TGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGG 360
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Db        301 TGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGG 360

Qy        361 ACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGG 420
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Qy        421 GCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGC 480
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Qy        481 CCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGG 540
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Db        481 CCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGG 540

Qy        541 CAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACA 600

Qy        601 GCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAAC 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAAC 660

Qy        661 CCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAG 720
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAG 720

Qy        721 TGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTA 780
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Db        721 TGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTA 780

Qy        781 AGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGC 840
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Qy        841 AACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGG 900
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Db        841 AACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGG 900

Qy        901 AGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACA 960
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Qy        961 AGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGG 1020
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Qy       1021 AGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATC 1080
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Qy       1081 TCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGG 1140
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Qy       1441 TGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGA 1500
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Qy        1921 CATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGGCAGCAG 1980
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Db        1921 CATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGGCAGCAG 1980

Qy        1981 GAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAATGAGGGCT 2040
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Qy        2101 TAGAACACATTTTATTTTCTTTTTCTTTCTTCATAAAGATGAGTAAAGTCTCAGTTTTCA 2160
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Qy        2161 CTGAGGGCAGGGAAAAGGAACACTCAGGTTTATTTTGA 2198
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Db        2161 CTGAGGGCAGGGAAAAGGAACACTCAGGTTTATTTTGA 2198


RESULT 2
AAH78799
ID   AAH78799 standard; cDNA; 2249 BP.
XX
AC   AAH78799;
XX
DT   08-MAR-2002  (first entry)
XX
DE   Human G-protein coupled receptor kinase 3 cDNA sequence.
XX
KW   G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
KW   drug screening; gene expression characterisation; NHP;
KW   novel human protein.
XX
OS   Homo sapiens.
XX
PN   WO200168869-A2.
XX
PD   20-SEP-2001.
XX
PF   08-MAR-2001; 2001WO-US007500.
XX
PR   10-MAR-2000; 2000US-0188449P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Walke DW,  Wilganowski NL,  Turner CA;
XX
DR   WPI; 2001-570872/64.
XX
PT   New polynucleotides encoding human proteins that share sequence
PT   similarity with animal kinases e.g. G-protein coupled receptor kinases,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Disclosure; Page 33-34; 34pp; English.
XX
CC   The present cDNA sequence encodes a human G-protein coupled receptor
CC   kinase (GRK), also designated NHP (novel human protein) in the
CC   specification, which is shown in the sequence listing. The invention
CC   comprises novel human nucleotide and protein sequences which have
CC   similarity to G-protein coupled receptor kinases. Oligonucleotides
```

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CC   derived from the nucleotides of the invention are useful as hybridisation
CC   probes for screening libraries and assessing gene expression patterns.
CC   The nucleotides of the invention are also useful in drug screening and
CC   gene therapy for the modulation of GRK expression. The nucleotides of the
CC   invention can be used to genetically engineer host cells to express GRK
CC   products in vivo. The nucleotide sequences of the invention are also
CC   useful in addressable arrays for identifying and characterising the
CC   temporal and tissue specific expression of a gene and in microarrays to
CC   screen collections of genetic material from patients who have a
CC   particular medical condition. The proteins of the invention are useful
CC   for generating antibodies, as reagents in diagnostic assays, for
CC   identifying other cellular gene products related to GRK, and as reagents
CC   in assays for screening for compounds that are useful in the treatment of
CC   mental, biological or medical disorders/diseases
XX
SQ   Sequence 2249 BP; 582 A; 577 C; 608 G; 482 T; 0 U; 0 Other;

  Query Match             91.4%;  Score 2008.8;  DB 4;  Length 2249;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         175 CAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAG 234
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         238 CAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAG 297

Qy         235 CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGG 294
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         298 CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGG 357

Qy         295 TGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGC 354
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         358 TGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGC 417

Qy         355 CCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGC 414
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         418 CCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGC 477

Qy         415 TGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGC 474
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         478 TGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGC 537

Qy         475 AGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCA 534
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         538 AGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCA 597

Qy         535 AGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCA 594
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         598 AGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCA 657

Qy         595 AAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACC 654
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         658 AAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACC 717

Qy         655 CGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAG 714
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         718 CGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAG 777

Qy         715 AGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGC 774
               |||||||||||||||||||||||  |||||||||||||||||||||||||||||||||||
Db         778 AGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGC 837

Qy         775 CCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCG 834
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         838 CCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCG 897

Qy         835 AGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTT 894
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         898 AGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTT 957

Qy         895 TTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAAC 954
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         958 TTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAAC 1017
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Qy          955 TGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAA 1014
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1018 TGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAA 1077

Qy         1015 TCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGA 1074
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1078 TCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGA 1137

Qy         1075 CCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACA 1134
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1138 CCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACA 1197

Qy         1135 ACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCT 1194
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1198 ACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCT 1257

Qy         1195 GTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATG 1254
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1258 GTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATG 1317

Qy         1255 TGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGA 1314
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1318 TGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGA 1377

Qy         1315 AGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCC 1374
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1378 AGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCC 1437

Qy         1375 TAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTT 1434
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1438 TAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTT 1497

Qy         1435 ATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGG 1494
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1498 ATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGG 1557

Qy         1495 ATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGG 1554
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1558 ATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGG 1617

Qy         1555 AAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCA 1614
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1618 AAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCA 1677

Qy         1615 GAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCC 1674
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1678 GAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCC 1737

Qy         1675 TGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAG 1734
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1738 TGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAG 1797

Qy         1735 ACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATA 1794
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1798 ACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATA 1857

Qy         1795 AGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTA 1854
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1858 AGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTA 1917

Qy         1855 TAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGG 1914
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1918 TAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGG 1977

Qy         1915 GTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGG 1974
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1978 GTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGG 2037

Qy         1975 CAGCAGGAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAATG 2034
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2038 CAGCAGGAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAATG 2097

Qy         2035 AGGGCTAATCAGTTAGGAGGGACATCACAACCACAAAACAATTCAAAAGACAGGCAAGCT 2094
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2098 AGGGCTAATCAGTTAGGAGGGACATCACAACCACAAAACAATTCAAAAGACAGGCAAGCT 2157

Qy         2095 CACTACTAGAACACATTTTATTTTCTTTTTCTTTCTTCATAAAGATGAGTAAAGTCTCAG 2154
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2158 CACTACTAGAACACATTTTATTTTCTTTTTCTTTCTTCATAAAGATGAGTAAAGTCTCAG 2217

Qy         2155 TTTTCACTGAGGGCAGGGAAAAGGAACACTCA 2186
                ||||||||||||||||||||||||||||||||
Db         2218 TTTTCACTGAGGGCAGGGAAAAGGAACACTCA 2249


RESULT 3
ACC44827
ID   ACC44827 standard; cDNA; 3186 BP.
XX
AC   ACC44827;
XX
DT   04-JUN-2003  (first entry)
XX
DE   Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:4.
XX
KW   Human; G protein coupled receptor kinase; GRK; cytostatic; antidiabetic;
KW   neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiant;
KW   vasotropic; antiasthmatic; gene therapy; cancer; diabetes; CNS disorder;
KW   central nervous system disorder; cardiovascular disorder; asthma; COPD;
KW   chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;
KW   Alzheimer's disease; Parkinson's disease; congestive heart failure;
KW   myocardial infarction; ischaemic disease; hypertensive vascular disease;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             85. .1746
FT                   /*tag=  a
FT                   /product= "G protein-coupled receptor kinase (GRK)"
XX
PN   WO2003018815-A2.
XX
PD   06-MAR-2003.
XX
PF   19-AUG-2002; 2002WO-EP009235.
XX
PR   21-AUG-2001; 2001US-0313464P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; 2003-278669/27.
DR   P-PSDB; ABP96709.
XX
PT   New G-protein coupled receptor kinase polypeptides and polynucleotides,
PT   useful in identifying modulators of the enzyme for treating cancer,
PT   diabetes, a central nervous system disorder, a cardiovascular disorder or
PT   asthma.
XX
PS   Claim 1; Fig 11; 129pp; English.
XX
CC   The present sequence encodes a human G protein-coupled receptor kinase
CC   (GRK) protein (I). (I) has cytostatic, antidiabetic, neuroprotective,
CC   nootropic, cardiovascular, anti-Parkinsonian, cardiant, vasotropic and
CC   antiasthmatic activities, and can be used in gene therapy. (I) can be
CC   regulated to treat cancer, diabetes, a central nervous system (CNS)
CC   disorder (e.g. anxiety or mood disorders, Alzheimer's disease and
CC   Parkinson's disease), cardiovascular disorders (e.g. congestive heart
CC   failure, myocardial infarction, ischaemic diseases of the heart or
CC   hypertensive vascular disease), asthma and chronic obstructive pulmonary
CC   disorder (COPD). GRK molecules are useful in screening for agents that
CC   regulate or decease the activity of a GRK. GRK sequences may also be used
CC   for detecting diseases and abnormalities or susceptibility to diseases
CC   and abnormalities related to the presence of mutations in the nucleic
CC   acid sequences that encode the GRK enzyme
XX
SQ   Sequence 3186 BP; 857 A; 737 C; 784 G; 808 T; 0 U; 0 Other;

  Query Match             90.5%;  Score 1988.8;  DB 7;  Length 3186;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1990;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        207 CGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCC 266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGTTGTCTCACCCGGGAAGGGAAAGCAGCCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCC 60

Qy        267 TGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGCC 326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGCC 120

Qy        327 AACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGG 386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGG 180

Qy        387 CGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTG 446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTG 240

Qy        447 TCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGAC 506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGAC 300

Qy        507 TTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAAC 566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAAC 360

Qy        567 TGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACT 626
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACT 420

Qy        627 TGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACC 686
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACC 480

Qy        687 AAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCT 746
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |||||||
Db        481 AAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCT 540

Qy        747 GAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTAC 806
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTAC 600

Qy        807 GACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACT 866
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACT 660

Qy        867 GAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAAC 926
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 GAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAAC 720

Qy        927 ACTGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGC 986
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACTGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGC 780

Qy        987 GAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTC 1046
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTC 840

Qy       1047 TCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAAT 1106
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAAT 900

Qy       1107 GGGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGG 1166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGG 960

Qy       1167 GTGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATC 1226
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 GTGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATC 1020

Qy       1227 GTCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTA 1286
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 GTCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTA 1080

Qy       1287 TCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGA 1346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 TCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGA 1140

Qy       1347 ACCAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTG 1406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ACCAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTG 1200

Qy       1407 GACTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAA 1466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GACTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAA 1260

Qy       1467 GATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTC 1526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTC 1320

Qy       1527 AAATTCCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCT 1586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AAATTCCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCT 1380

Qy       1587 AAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAAGTCTGATGATCCCAGGAAACATCAT 1646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAAGTCTGATGATCCCAGGAAACATCAT 1440

Qy       1647 TTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTG 1706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTG 1500

Qy       1707 CCAGACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTT 1766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 CCAGACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTT 1560

Qy       1767 CGGGGGGTGGAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCT 1826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 CGGGGGGTGGAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCT 1620

Qy       1827 GTTCCTATAGCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGAC 1886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 GTTCCTATAGCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGAC 1680

Qy       1887 CCCAACAGACCTACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTA 1946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CCCAACAGACCTACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTA 1740

Qy       1947 TTGTAAATTGCTCTCTTTACCAGACAGGCAGCAGGAGTCTCGGCTGACATAATCCTCGAA 2006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 TTGTAAATTGCTCTCTTTACCAGACAGGCAGCAGGAGTCTCGGCTGACATAATCCTCGAA 1800

Qy       2007 TGTTCCACACGTGGAAATCTGTGGAATGAGGGCTAATCAGTTAGGAGGGACATCACAACC 2066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TGTTCCACACGTGGAAATCTGTGGAATGAGGGCTAATCAGTTAGGAGGGACATCACAACC 1860

Qy       2067 ACAAAACAATTCAAAAGACAGGCAAGCTCACTACTAGAACACATTTTATTTTCTTTTTCT 2126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 ACAAAACAATTCAAAAGACAGGCAAGCTCACTACTAGAACACATTTTATTTTCTTTTTCT 1920

Qy       2127 TTCTTCATAAAGATGAGTAAAGTCTCAGTTTTCACTGAGGGCAGGGAAAAGGAACACTCA 2186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 TTCTTCATAAAGATGAGTAAAGTCTCAGTTTTCACTGAGGGCAGGGAAAAGGAACACTCA 1980

Qy       2187 GGTTTATTTTGA 2198
              ||||||||||||
Db       1981 GGTTTATTTTGA 1992


RESULT 4
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ADC39221
ID   ADC39221 standard; cDNA; 1821 BP.
XX
AC   ADC39221;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Novel human NOVX polypeptide coding sequence SEQ ID NO: 165.
XX
KW   ds; gene; antidiabetic; cytostatic; immunomodulator; anorectic;
KW   antilipemic; nootropic; neuroprotective; immunostimulant;
KW   antiparkinsonian; anti-HIV; antiasthmatic; antiinflammatory; hypotensive;
KW   antiarteriosclerotic; hemostatic; osteopathic; gene therapy.; NOVX;
KW   diabetes; obesity; cancer; lymphoma; uterus cancer; prostate cancer;
KW   dyslipidemia; anorexia; wasting disorder; Alzheimer's disease;
KW   Parkinson's disorder; cachexia; cardiomyopathy; AIDS; asthma;
KW   Crohn's disease; multiple sclerosis; hypertension; atherosclerosis;
KW   hemophilia; graft-versus-host disease;
KW   Albright hereditary osteodystrophy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             73. .1732
FT                   /*tag=  a
XX
PN   WO2003010327-A2.
XX
PD   06-FEB-2003.
XX
PF   02-MAY-2002; 2002WO-US014199.
XX
PR   02-MAY-2001; 2001US-0288063P.
PR   03-MAY-2001; 2001US-0288395P.
PR   07-MAY-2001; 2001US-0289087P.
PR   09-MAY-2001; 2001US-0289817P.
PR   09-MAY-2001; 2001US-0289818P.
PR   11-MAY-2001; 2001US-0290194P.
PR   14-MAY-2001; 2001US-0290753P.
PR   15-MAY-2001; 2001US-0291181P.
PR   16-MAY-2001; 2001US-0291243P.
PR   18-MAY-2001; 2001US-0292001P.
PR   21-MAY-2001; 2001US-0292374P.
PR   22-MAY-2001; 2001US-0292587P.
PR   23-MAY-2001; 2001US-0293107P.
PR   25-MAY-2001; 2001US-0293747P.
PR   29-MAY-2001; 2001US-0294109P.
PR   29-MAY-2001; 2001US-0294110P.
PR   30-MAY-2001; 2001US-0294434P.
PR   31-MAY-2001; 2001US-0294827P.
PR   12-JUL-2001; 2001US-0304879P.
PR   31-JUL-2001; 2001US-0308901P.
PR   14-AUG-2001; 2001US-0312270P.
PR   17-AUG-2001; 2001US-0313416P.
PR   10-SEP-2001; 2001US-0318463P.
PR   27-SEP-2001; 2001US-0325683P.
PR   18-OCT-2001; 2001US-0330292P.
PR   28-NOV-2001; 2001US-0333873P.
PR   03-DEC-2001; 2001US-0336909P.
PR   03-DEC-2001; 2001US-0337552P.
PR   21-FEB-2002; 2002US-0359245P.
PR   01-MAY-2002; 2002US-00136826.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Miller CE,  Kekuda R,  Malyankar UM,  Li L,  Pena CEA,  Spytek KA;
PI   Gorman L,  Guo X,  Fernandes ER,  Smithson G,  Stone DJ,  Zerhusen BD;
PI   Patturajan M,  Anderson DW,  Mezes PS,  Peyman JA,  Macdougall JR;
PI   Padigaru M,  Rastelli L,  Shenoy SG,  Gerlach VL,  Shimkets RA,  Zhong M;
PI   Edinger SR,  Ellerman K;
XX
DR   WPI; 2003-239445/23.
DR   P-PSDB; ADC39222.
XX
PT   New NOVX polypeptides and polynucleotides, useful in gene therapy,
PT   particularly for treating or preventing a syndrome associated with a
PT   human disease e.g. diabetes, obesity, cancer, Alzheimer's disease,
PT   hypertension or hemophilia.
XX
PS   Claim 20; SEQ ID NO 165; 748pp; English.
XX
CC   The invention relates to new isolated NOVX polypeptides, the genes
CC   encoding them or sequences having at least 95% identity to the amino acid
CC   or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic,
CC   particularly in the manufacture of a medicament for treating a syndrome
CC   associated with a human disease, which includes a pathology associated
CC   with NOVX polypeptide. The NOVX polypeptide is particularly useful for
CC   treating, preventing or alleviating pathology associated with NOVX
CC   polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and
CC   polypeptide are especially useful for treating or preventing e.g.
CC   diabetes, obesity, cancers (e.g. lymphoma, uterus cancer or prostate
CC   cancer), dyslipidemias, anorexia, wasting disorders, Alzheimer's disease,
CC   Parkinson's disorder, cachexia, cardiomyopathy, AIDS, asthma, Crohn's
CC   disease, multiple sclerosis, hypertension, atherosclerosis, hemophilia,
CC   graft-versus-host disease or Albright hereditary osteodystrophy. The DNA
CC   encoding the protein is useful in gene therapy for treating the above
CC   conditions. These are also useful in developing powerful assay system for
CC   functional analysis of various human disorders, as well as in diagnostic
CC   applications. This sequence represents one of the NOVX genes of the
CC   invention.
XX
SQ   Sequence 1821 BP; 453 A; 459 C; 524 G; 385 T; 0 U; 0 Other;

  Query Match             82.7%;  Score 1817.8;  DB 9;  Length 1821;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1819;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        219 CGGGAAGGGAAAGCAGCCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCC 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CGGGAAGGGAAAGCAGCCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCC 60

Qy        279 CCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTAC 338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTAC 120

Qy        339 CTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGC 398
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGC 180

Qy        399 CTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTC 458
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTC 240

Qy        459 CACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACA 518
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACA 300

Qy        519 GTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCC 578
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCC 360

Qy        579 GAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCC 638
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCC 420

Qy        639 CCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCA 698
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCA 480

Qy        699 GCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCT 758
              |||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||
Db        481 GCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCT 540

Qy        759 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 818
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 600
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Qy       819 CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 878
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 660

Qy       879 CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG 938
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG 720

Qy       939 TATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCT 998
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 TATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCT 780

Qy       999 CTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTAT 1058
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTAT 840

Qy      1059 GCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTC 1118
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       841 GCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTC 900

Qy      1119 AAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTAC 1178
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 AAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTAC 960

Qy      1179 TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 1238
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 1020

Qy      1239 ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1298
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1080

Qy      1299 CTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTAC 1358
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 CTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTAC 1140

Qy      1359 ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1418
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1200

Qy      1419 ATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAA 1478
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 ATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAA 1260

Qy      1479 AAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCAT 1538
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 AAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCAT 1320

Qy      1539 GATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAG 1598
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 GATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAG 1380

Qy      1599 CAACGCTTAGGAAGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACG 1658
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 CAACGCTTAGGAAGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACG 1440

Qy      1659 ATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCA 1718
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 ATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCA 1500

Qy      1719 GTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAA 1778
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 GTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAA 1560

Qy      1779 TTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCA 1838
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 TTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCA 1620

Qy      1839 TGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCT 1898
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1621 TGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCT 1680

Qy      1899 ACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCT 1958
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1681 ACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCT 1740

Qy      1959 CTCTTTACCAGACAGGCAGCAGGAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGT 2018
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1741 CTCTTTACCAGACAGGCAGCAGGAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGT 1800

Qy      2019 GGAAATCTGTGGAATGAGGGC 2039
             |||||||||||||||||||||
Db      1801 GGAAATCTGTGGAATGAGGGC 1821


RESULT 5
ABZ56943
ID   ABZ56943 standard; DNA; 1761 BP.
XX
AC   ABZ56943;
XX
DT   04-APR-2003  (first entry)
XX
DE   Human gene sequence relative to the invention # SEQ ID 11.
XX
KW   Human; heart disease; cancer; omentopathy; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             26..1687
FT                   /*tag=  a
XX
PN   WO2002103020-A1.
XX
PD   27-DEC-2002.
XX
PF   14-JUN-2002; 2002WO-JP005942.
XX
PR   15-JUN-2001; 2001JP-00182654.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Koyama N,  Tanida S,  Yamamoto K;
XX
DR   WPI; 2003-157045/15.
DR   P-PSDB; ABP60079.
XX
PT   Novel disease-associated gene of the RGS gene family and its product,
PT   applicable in diagnosis of and screening for drugs for heart diseases,
PT   cancers and omentopathy.
XX
PS   Example 3; Page 85-86; 96pp; Japanese.
XX
CC   The invention relates to a novel disease associated gene and its uses.
CC   The gene and its encoded protein are useful for diagnosis of and
CC   screening for drugs for heart diseases, cancers and omentopathy. The
CC   current sequence represents a human gene sequence relative to the
CC   invention
XX
SQ   Sequence 1761 BP; 441 A; 441 C; 504 G; 375 T; 0 U; 0 Other;

  Query Match             80.0%;  Score 1757.8;  DB 7;  Length 1761;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1759;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy       266 CTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGC 325
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 CTGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGC 60

Qy       326 CAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCG 385
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 CAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCG 120

Qy       386 GCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCT 445
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCT 180

Qy        446 GTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGA 505
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGA 240

Qy        506 CTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAA 565
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAA 300

Qy        566 CTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCAC 625
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCAC 360

Qy        626 TTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCAC 685
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCAC 420

Qy        686 CAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGC 745
              ||||||||||||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        421 CAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGC 480

Qy        746 TGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTA 805
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 TGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTA 540

Qy        806 CGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCAC 865
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCAC 600

Qy        866 TGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAA 925
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAA 660

Qy        926 CACTGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGG 985
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CACTGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGG 720

Qy        986 CGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGT 1045
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 CGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGT 780

Qy       1046 CTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAA 1105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAA 840

Qy       1106 TGGGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCG 1165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGGGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCG 900

Qy       1166 GGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCAT 1225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCAT 960

Qy       1226 CGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTT 1285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTT 1020

Qy       1286 ATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGG 1345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGG 1080

Qy       1346 AACCAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGT 1405
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 AACCAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGT 1140

Qy       1406 GGACTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAA 1465
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GGACTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAA 1200

Qy       1466 AGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGT 1525
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1201 AGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGT 1260

Qy       1526 CAAATTCCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGC 1585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CAAATTCCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGC 1320

Qy       1586 TAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAAGTCTGATGATCCCAGGAAACATCA 1645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAAGTCTGATGATCCCAGGAAACATCA 1380

Qy       1646 TTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGT 1705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGT 1440

Qy       1706 GCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGT 1765
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 GCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGT 1500

Qy       1766 TCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGC 1825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 TCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGC 1560

Qy       1826 TGTTCCTATAGCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGA 1885
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 TGTTCCTATAGCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGA 1620

Qy       1886 CCCCAACAGACCTACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTT 1945
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1621 CCCCAACAGACCTACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTT 1680

Qy       1946 ATTGTAAATTGCTCTCTTTACCAGACAGGCAGCAGGAGTCTCGGCTGACATAATCCTCGA 2005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ATTGTAAATTGCTCTCTTTACCAGACAGGCAGCAGGAGTCTCGGCTGACATAATCCTCGA 1740

Qy       2006 ATGTTCCACACGTGGAAATCT 2026
              |||||||||||||||||||||
Db       1741 ATGTTCCACACGTGGAAATCT 1761


RESULT 6
ABQ86178
ID   ABQ86178 standard; DNA; 1662 BP.
XX
AC   ABQ86178;
XX
DT   10-SEP-2002  (first entry)
XX
DE   Novel human gene. SEQ ID 49.
XX
KW   Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian;
KW   nootropic; neuroprotective; immunosuppressive; haemostatic;
KW   antiinflammatory; cardiant; antiulcer; virucide; antithyroid;
KW   cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW   wound healing disorders; atherosclerosis; Parkinson's disease;
KW   Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW   inflammation; neoplastic disease; nervous system disorder;
KW   cardiovascular disorders; pancreatitis; respiratory disorder;
KW   hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW   developmental abnormality; gastrointestinal ulceration; neuropathy;
KW   haematological disease; metabolic disease; sperm dysfunction;
KW   thyroid disorder; hypothyroidism; brain damage; colitis;
KW   cone photo- transduction deficiency; neurological disease; stroke;
KW   angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
KW   trachea; thymus; lymph node; muscular system; obesity; anorexia;
KW   growth abnormality; precocious puberty; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200250105-A1.
XX
PD   27-JUN-2002.
XX
PF   17-DEC-2001; 2001WO-US049232.
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XX
PR   19-DEC-2000; 2000US-0256710P.
PR   20-DEC-2000; 2000US-0257048P.
PR   09-JAN-2001; 2001US-0260482P.
PR   30-JAN-2001; 2001US-0264922P.
PR   06-FEB-2001; 2001US-0266797P.
PR   19-MAR-2001; 2001US-0276988P.
PR   04-APR-2001; 2001US-0281535P.
PR   08-MAY-2001; 2001US-0289622P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Agarwal P,  Birkeland M,  Cogswell JP,  Kabnick KF,  Lai Y;
PI   Martensen SA,  Rizvi SK,  Smith RF,  Strum JC,  Xie Q;
XX
DR   WPI; 2002-508784/54.
DR   P-PSDB; ABP61013.
XX
PT   Secreted proteins and polynucleotides useful as vaccines for preventing
PT   or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT   Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
XX
PS   Claim 2(a); Page 255-256; 335pp; English.
XX
CC   The invention relates to an isolated polypeptide with signal sequences
CC   which allow it to be secreted extracellularly or membrane associated. The
CC   activity of polypeptides of the invention may be described as,
CC   cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic,
CC   neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
CC   cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic,
CC   and metabolic. Polypeptides and polynucleotides of the invention are
CC   useful in the treatment, or as a vaccine in the prevention of, cancer,
CC   wound healing disorders, infection, atherosclerosis, Parkinson's disease
CC   and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
CC   inflammation, neoplastic diseases, nervous system related disorders and
CC   cardiovascular disorders, pancreatitis, respiratory disorder,
CC   hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC   developmental abnormality, gastrointestinal ulceration, neuropathy,
CC   haematological diseases, metabolic diseases, sperm dysfunction, thyroid
CC   disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC   transduction deficiency, neurological diseases, stroke, angiogenesis,
CC   ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC   trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC   growth abnormalities, and alleviation of precocious puberty. The
CC   sequences given in records ABQ86130-ABQ86184 represent novel human cDNA's
CC   of the invention
XX
SQ   Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

  Query Match             75.5%;  Score 1658.8;  DB 6;  Length 1662;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1660;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy         591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy         651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy         711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
               |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db         421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy         771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy         831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy         891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy         951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
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Db         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
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Db         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
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Db        1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
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Qy       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
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Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
              ||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662

RESULT 7
AAD26466
ID   AAD26466 standard; cDNA; 1662 BP.
XX
AC   AAD26466;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human kinase PKIN-19 cDNA.
XX
KW   Human; kinase; PKIN-19; cancer; leukaemia; adenocarcinoma; osteoporosis;
KW   immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW   Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW   allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW   autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
KW   Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
KW   rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
KW   hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
KW   cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW   congestive heart failure; ischaemic heart disease; lung tumour; gout;
KW   fatty liver; Niemann-Pick's disease; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "Human PKIN-19 protein"
XX
PN   WO200196547-A2.
XX
PD   20-DEC-2001.
XX
PF   14-JUN-2001; 2001WO-US019444.
XX
PR   15-JUN-2000; 2000US-0212073P.
PR   23-JUN-2000; 2000US-0213467P.
PR   30-JUN-2000; 2000US-0215651P.
PR   07-JUL-2000; 2000US-0216605P.
PR   13-JUL-2000; 2000US-0218372P.
PR   25-AUG-2000; 2000US-0228056P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yue H,  Lal P,  Bandman O,  Borowsky ML,  Au-Young J,  Lu Y;
PI   Gandhi AR,  Tribouley CM,  Walia NK,  Yao MG,  Lu DAM,  Greenwald SR;
PI   Ramkumar J,  Griffin JA,  Kearney L,  Burford N,  Nguyen DB,  Tang YT;
PI   Baughn MR,  He A,  Thornton M,  Hafalia A,  Patterson C,  Gururajan R;
PI   Lo TP,  Khan F,  Recipon SA,  Azimzai Y,  Policky JL,  Ding L;
PI   Grether M,  Elliott VS,  Thangavelu K,  Batra S,  Ison CH;
XX
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DR   WPI; 2002-090207/12.
DR   P-PSDB; AAE16273.
XX
PT   New polypeptides, useful for diagnosing, treating or preventing disorders
PT   of growth and development, cardiovascular and lipid, and diseases such as
PT   cancer, comprise human kinase polypeptides.
XX
PS   Claim 5; Page 190; 197pp; English.
XX
CC   The invention relates to human kinase PKIN proteins and their
CC   corresponding cDNAs. A composition containing PKIN agonist is useful for
CC   treating a disease or condition associated with decreased expression of
CC   PKIN and a composition comprising PKIN antagonist is useful for treating
CC   a disease or condition associated with overexpression of PKIN. The
CC   disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
CC   myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder
CC   (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
CC   atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
CC   autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
CC   mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
CC   osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
CC   rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
CC   bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
CC   growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
CC   Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
CC   vascular disease (arteriovenous fistula, hypertension, vasculitis,
CC   aneurysms, congestive heart failure, angina pectoris, myocarditis,
CC   ischaemic heart disease, chronic bronchitis, lung tumours); lipid
CC   disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
CC   hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
CC   of a test compound and in gene therapy. The present sequence is human
CC   PKIN-19 cDNA
XX
SQ   Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

  Query Match             75.5%;  Score 1658.8;  DB 6;  Length 1662;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1660;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
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Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
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Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
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Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
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Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
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Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
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Qy       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
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Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
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Qy       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
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Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
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Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

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Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
```

```
Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
              ||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662

RESULT 8
AAD46350
ID   AAD46350 standard; cDNA; 1662 BP.
XX
AC   AAD46350;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Human cone opsin kinase (GRK7) cDNA.
XX
KW   Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
KW   GRK7; cone visual signalling; visual sensitivity; visual resolution;
KW   night blindness; colour blindness; Oguchi disease; Pineal gland activity;
KW   chronobiological desynchrony; depression; anxiety; memory loss; headache;
KW   mental fogginess; fatigue; jet lag; circadian rhythm; ophthalmological;
KW   gene therapy; antidepressant; analgesic; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "Human GRK7 protein"
XX
PN   WO200272541-A2.
XX
PD   19-SEP-2002.
XX
PF   07-MAR-2002; 2002WO-US007025.
XX
PR   07-MAR-2001; 2001US-0274006P.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Bird TA,  Spencer M,  Mosley BA;
XX
DR   WPI; 2002-723307/78.
DR   P-PSDB; AAE28952.
XX
PT   Identifying compounds that alter inhibition of cone opsin kinase
PT   polypeptide activity for treating a conditions related to cone visual
PT   signaling, comprises mixing a compound with a cone opsin kinase and with
PT   an inhibitory polypeptide.
XX
PS   Example 4; Page 45-46; 61pp; English.
XX
CC   The present invention relates to novel human cone opsin kinase (G-protein
CC   coupled receptor kinase 7; GRK7) and their corresponding polynucleotides.
CC   The invention further relates to a method of identifying compounds that
CC   alter the inhibition of GRK7 polypeptide activity which involves mixing a
CC   test compound with GRK7 protein and an inhibitory polypeptide and
CC   determining if the test compound alters the inhibition of GRK7 protein
CC   activity by the inhibitory polypeptide. GRk7 sequences are useful for
CC   treating conditions related to cone visual signalling (e.g., night
CC   blindness, colour blindness, difficulty with colour vision, visual
CC   sensitivity, visual resolution or in adapting to changes in light
CC   intensity, Oguchi disease or dominant congenital stationary night
CC   blindness), Pineal gland activity (e.g., chronobiological desynchrony,
CC   depression, anxiety, mental fogginess, memory loss, headaches, fatigue,
CC   or jet lag). Agonists of GRK7 polypeptide activity may be used to treat
CC   or ameliorate symptoms of a disease for which increased GRK7 polypeptide
CC   activity is beneficial, e.g., decreased colour sensitivity or other cone
CC   photoreceptor-mediated diseases. The GRK7 proteins are also useful in the
CC   preparation of a medicament for treating a condition or disease related
CC   to cone photoreceptor visual signaling or circadian rhythm, as molecular
CC   probes to screen for inherited defects in colour vision, circadian rhythm
CC   and vision resolution. They are also used as gene therapy tools for
CC   individuals with such disorders. The present sequence is human GRK7 cDNA
XX
SQ   Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

  Query Match             75.5%;  Score 1658.8;  DB 6;  Length 1662;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1660;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
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Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
              ||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662


RESULT 9
AAH78797
ID   AAH78797 standard; cDNA; 1662 BP.
XX
AC   AAH78797;
XX
DT   08-MAR-2002  (first entry)
XX
DE   Human G-protein coupled receptor kinase 1 cDNA sequence.
XX
KW   G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
KW   drug screening; gene expression characterisation; NHP;
KW   novel human protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "G-protein coupled receptor kinase 1"
XX
PN   WO200168869-A2.
XX
PD   20-SEP-2001.
XX
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```
PF   08-MAR-2001; 2001WO-US007500.
XX
PR   10-MAR-2000; 2000US-0188449P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Walke DW,  Wilganowski NL,  Turner CA;
XX
DR   WPI; 2001-570872/64.
DR   P-PSDB; AAG77815.
XX
PT   New polynucleotides encoding human proteins that share sequence
PT   similarity with animal kinases e.g. G-protein coupled receptor kinases,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Claim 1; Page 30; 34pp; English.
XX
CC   The present cDNA sequence encodes a human G-protein coupled receptor
CC   kinase (GRK), also designated NHP (novel human protein) in the
CC   specification, which is claimed in the invention. The invention comprises
CC   novel human nucleotide and protein sequences which have similarity to G-
CC   protein coupled receptor kinases. Oligonucleotides derived from the
CC   nucleotides of the invention are useful as hybridisation probes for
CC   screening libraries and assessing gene expression patterns. The
CC   nucleotides of the invention are also useful in drug screening and gene
CC   therapy for the modulation of GRK expression. The nucleotides of the
CC   invention can be used to genetically engineer host cells to express GRK
CC   products in vivo. The nucleotide sequences of the invention are also
CC   useful in addressable arrays for identifying and characterising the
CC   temporal and tissue specific expression of a gene and in microarrays to
CC   screen collections of genetic material from patients who have a
CC   particular medical condition. The proteins of the invention are useful
CC   for generating antibodies, as reagents in diagnostic assays, for
CC   identifying other cellular gene products related to GRK, and as reagents
CC   in assays for screening for compounds that are useful in the treatment of
CC   mental, biological or medical disorders/diseases
XX
SQ   Sequence 1662 BP; 420 A; 410 C; 479 G; 352 T; 0 U; 1 Other;

  Query Match             75.5%;  Score 1658.4;  DB 4;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1659;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
              |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
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Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
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Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662


RESULT 10
AAD28071
ID   AAD28071 standard; cDNA; 1662 BP.
XX
AC   AAD28071;
XX
DT   22-APR-2002  (first entry)
XX
DE   Human kinase cDNA.
XX
KW   Human; kinase; G-protein coupled receptor kinase; tissue differentiation;
KW   chromosome 3; therapeutic; immune response; drug screening; enzyme; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "Human kinase protein"
XX
PN   WO200192496-A2.
XX
PD   06-DEC-2001.
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PF   31-MAY-2001; 2001WO-US017510.
XX
PR   01-JUN-2000; 2000US-0208331P.
PR   18-DEC-2000; 2000US-00738894.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Guegler K,  Di Francesco V,  Beasley EM;
XX
DR   WPI; 2002-130533/17.
DR   P-PSDB; AAE17136.
XX
PT   New isolated human kinase proteins and nucleic acids, useful as a major
PT   target for drug action and development, particularly for screening
PT   modulators of the kinase peptides.
XX
PS   Claim 4; Fig 1; 87pp; English.
XX
CC   The invention relates to human kinase proteins that are related to G-
CC   protein coupled receptor kinase subfamily. Human kinase gene is located
CC   on chromosome 3. The kinase peptide and nucleic acid are useful in the
CC   development of human therapeutic and diagnostic compositions. The peptide
CC   is useful as a major target for drug action and development, and is
CC   valuable to the field of pharmaceutical development to identify and
CC   characterise modulators of the kinase. The proteins may also be used to
CC   raise antibodies or to elicit an immune response, as a reagent in assays
CC   designed to quantitatively determine levels of the protein in biological
CC   fluids and as markers for tissues in which the corresponding protein is
CC   preferentially expressed (either constitutively or at a particular stage
CC   of tissue differentiation or development or in a disease state). The
CC   kinase proteins are also useful for providing a target for diagnosing a
CC   disease or predisposition to disease mediated by the peptide. The nucleic
CC   acid molecules are useful for probes, primers, chemical intermediates and
CC   in biological assays. The nucleic acids are also useful in making vectors
CC   containing the gene regulatory regions of the nucleic acid molecules and
CC   for drug screening to identify compounds that modulate kinase nucleic
CC   acid expression. The present sequence is human kinase cDNA expressed in
CC   skins, germinal center B cells, colon, kidney and lung
```

```
XX
SQ   Sequence 1662 BP; 419 A; 411 C; 480 G; 352 T; 0 U; 0 Other;

  Query Match             75.4%;  Score 1657.2;  DB 6;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1659;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
              ||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662


RESULT 11
AAS06702
ID   AAS06702 standard; cDNA; 1662 BP.
XX
AC   AAS06702;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Polynucleotide sequence encoding human protein kinase #2.
XX
KW   Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW   metabolic disorder; immune related disease; neurological disorder;
KW   neurodegenerative disorder; inflammatory disorder; infectious disease;
KW   reproductive disorder; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138503-A2.
XX
PD   31-MAY-2001.
XX
PF   22-NOV-2000; 2000WO-US032085.
XX
PR   24-NOV-1999;   99US-0167482P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD,  Whyte D,  Manning G,  Sudarsanam S,  Martinez R;
PI   Flanagan P,  Clary D;
XX
DR   WPI; 2001-343950/36.
DR   P-PSDB; AAU03502.
XX
PT   Nucleic acids encoding human kinase polypeptides, useful for preventing
PT   diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT   neuronal-associated diseases, and microbial infections.
XX
PS   Example 1; Fig 1; 433pp; English.
XX
CC   AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
CC   protein kinases have been identified as members of the tyrosine or
CC   serine/threonine kinase (PTK and STK) families. The polynucleotides
CC   encoding protein kinases and the polypeptides may be used in the
CC   prevention, diagnosis and treatment of diseases associated with
CC   inappropriate kinase expression. For example, they may be used to treat
CC   cancers (especially cancers of haematopoietic origin), cardiovascular
CC   disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC   immune related diseases (e.g. rheumatoid arthritis), neurological
CC   disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC   Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC   disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC   Additionally, polynucleotides encoding protein kinases may be used for
CC   gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC   polypeptides may be used as antigens in the production of antibodies
CC   against the protein kinases and in assays to identify modulators of
CC   protein kinase expression and activity
XX
SQ   Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;

  Query Match             75.3%;  Score 1655.6;  DB 4;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1658;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
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Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGGGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAAGA 1320

Qy       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
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              ||||||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662

RESULT 12
ACC44826
ID   ACC44826 standard; cDNA; 1662 BP.
XX
AC   ACC44826;
XX
DT   04-JUN-2003  (first entry)
XX
DE   Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:1.
XX
KW   Human; G protein coupled receptor kinase; GRK; cytostatic; antidiabetic;
KW   neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiant;
KW   vasotropic; antiasthmatic; gene therapy; cancer; diabetes; CNS disorder;
KW   central nervous system disorder; cardiovascular disorder; asthma; COPD;
KW   chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;
KW   Alzheimer's disease; Parkinson's disease; congestive heart failure;
KW   myocardial infarction; ischaemic disease; hypertensive vascular disease;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "G protein-coupled receptor kinase (GRK)"
XX
PN   WO2003018815-A2.
XX
PD   06-MAR-2003.
XX
PF   19-AUG-2002; 2002WO-EP009235.
XX
PR   21-AUG-2001; 2001US-0313464P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; 2003-278669/27.
DR   P-PSDB; ABP96707.
XX
PT   New G-protein coupled receptor kinase polypeptides and polynucleotides,
PT   useful in identifying modulators of the enzyme for treating cancer,
PT   diabetes, a central nervous system disorder, a cardiovascular disorder or
PT   asthma.
XX
PS   Claim 1; Fig 1; 129pp; English.
XX
CC   The present sequence encodes a human G protein-coupled receptor kinase
CC   (GRK) protein (I). (I) has cytostatic, antidiabetic, neuroprotective,
CC   nootropic, cardiovascular, anti-Parkinsonian, cardiant, vasotropic and
CC   antiasthmatic activities, and can be used in gene therapy. (I) can be
CC   regulated to treat cancer, diabetes, a central nervous system (CNS)
CC   disorder (e.g. anxiety or mood disorders, Alzheimer's disease and
CC   Parkinson's disease), cardiovascular disorders (e.g. congestive heart
CC   failure, myocardial infarction, ischaemic diseases of the heart or
CC   hypertensive vascular disease), asthma and chronic obstructive pulmonary
CC   disorder (COPD). GRK molecules are useful in screening for agents that
CC   regulate or decease the activity of a GRK. GRK sequences may also be used
CC   for detecting diseases and abnormalities or susceptibility to diseases
CC   and abnormalities related to the presence of mutations in the nucleic
CC   acid sequences that encode the GRK enzyme
XX
SQ   Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;

  Query Match             75.3%;  Score 1655.6;  DB 7;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1658;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
```

```
Qy    291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy    351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy    411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy    471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy    531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy    591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy    651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy    711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
          |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db    421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy    771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy    831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy    891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy    951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy   1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy   1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy   1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy   1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy   1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
          |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961 AATGGGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy   1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy   1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy   1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy   1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy   1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db   1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAAGA 1320

Qy   1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy   1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy   1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy   1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy   1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy   1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
          ||||||||||||||||||||||||||||||||||||||||||
Db   1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662


RESULT 13
ABZ56934
ID   ABZ56934 standard; DNA; 1191 BP.
XX
AC   ABZ56934;
XX
DT   04-APR-2003  (first entry)
XX
DE   Human RGSNo9 encoding DNA # SEQ ID 2.
XX
KW   Human; RGSNo9; heart disease; cancer; omentopathy; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1191
FT                   /*tag=  a
FT                   /product= "RGSNo9"
XX
PN   WO2002103020-A1.
XX
PD   27-DEC-2002.
XX
PF   14-JUN-2002; 2002WO-JP005942.
XX
PR   15-JUN-2001; 2001JP-00182654.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Koyama N,  Tanida S,  Yamamoto K;
XX
DR   WPI; 2003-157045/15.
DR   P-PSDB; ABP60078.
```

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XX
PT   Novel disease-associated gene of the RGS gene family and its product,
PT   applicable in diagnosis of and screening for drugs for heart diseases,
PT   cancers and omentopathy.
XX
PS   Claim 6; Page 81-82; 96pp; Japanese.
XX
CC   The invention relates to a novel disease associated gene and its uses.
CC   The gene and its encoded protein are useful for diagnosis of and
CC   screening for drugs for heart diseases, cancers and omentopathy. The
CC   current sequence represents the human RGSNo9 encoding DNA sequence
XX
SQ   Sequence 1191 BP; 274 A; 320 C; 363 G; 234 T; 0 U; 0 Other;

  Query Match             54.0%;  Score 1187.8;  DB 7;  Length 1191;
  Best Local Similarity   99.8%;  Pred. No. 6.3e-297;
  Matches 1189;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
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Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
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Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAG 1481
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAG 1191


RESULT 14
AAD46351
ID   AAD46351 standard; cDNA; 1486 BP.
XX
AC   AAD46351;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Human cone opsin kinase (GRK7) OK6 splice variant cDNA.
XX
KW   Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
KW   GRK7; cone visual signalling; visual sensitivity; visual resolution;
KW   night blindness; colour blindness; Oguchi disease; Pineal gland activity;
KW   chronobiological desynchrony; depression; anxiety; memory loss; headache;
KW   mental fogginess; fatigue; jet lag; circadian rhythm; ophthalmological;
KW   gene therapy; antidepressant; analgesic; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1062
FT                   /*tag=  a
FT                   /product= "Human GRK7 OK6 splice variant protein"
XX
PN   WO200272541-A2.
XX
PD   19-SEP-2002.
XX
PF   07-MAR-2002; 2002WO-US007025.
XX
PR   07-MAR-2001; 2001US-0274006P.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Bird TA,  Spencer M,  Mosley BA;
XX
DR   WPI; 2002-723307/78.
DR   P-PSDB; AAE28953.
XX
PT   Identifying compounds that alter inhibition of cone opsin kinase
PT   polypeptide activity for treating a conditions related to cone visual
PT   signaling, comprises mixing a compound with a cone opsin kinase and with
PT   an inhibitory polypeptide.
XX
PS   Example 4; Page 48-49; 61pp; English.
XX
CC   The present invention relates to novel human cone opsin kinase (G-protein
CC   coupled receptor kinase 7; GRK7) and their corresponding polynucleotides.
CC   The invention further relates to a method of identifying compounds that
CC   alter the inhibition of GRK7 polypeptide activity which involves mixing a
CC   test compound with GRK7 protein and an inhibitory polypeptide and
CC   determining if the test compound alters the inhibition of GRK7 protein
CC   activity by the inhibitory polypeptide. GRk7 sequences are useful for
CC   treating conditions related to cone visual signalling (e.g., night
CC   blindness, colour blindness, difficulty with colour vision, visual
CC   sensitivity, visual resolution or in adapting to changes in light
CC   intensity, Oguchi disease or dominant congenital stationary night
CC   blindness), Pineal gland activity (e.g., chronobiological desynchrony,
CC   depression, anxiety, mental fogginess, memory loss, headaches, fatigue,
CC   or jet lag). Agonists of GRK7 polypeptide activity may be used to treat
CC   or ameliorate symptoms of a disease for which increased GRK7 polypeptide
CC   activity is beneficial, e.g., decreased colour sensitivity or other cone
CC   photoreceptor-mediated diseases. The GRK7 proteins are also useful in the
CC   preparation of a medicament for treating a condition or disease related
CC   to cone photoreceptor visual signaling or circadian rhythm, as molecular
CC   probes to screen for inherited defects in colour vision, circadian rhythm
CC   and vision resolution. They are also used as gene therapy tools for
CC   individuals with such disorders. The present sequence is human GRK7 OK6
CC   splice variant cDNA
XX
SQ   Sequence 1486 BP; 353 A; 387 C; 434 G; 312 T; 0 U; 0 Other;

  Query Match             53.2%;  Score 1170.4;  DB 6;  Length 1486;
  Best Local Similarity   83.9%;  Pred. No. 2.2e-292;
  Matches 1459;  Conservative    0;  Mismatches    6;  Indels  275;  Gaps    1;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
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Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

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Qy       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
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RESULT 15
AAH78798
ID   AAH78798 standard; cDNA; 1062 BP.
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AC   AAH78798;
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DT   08-MAR-2002  (first entry)
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DE   Human G-protein coupled receptor kinase 2 cDNA sequence.
XX
KW   G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
KW   drug screening; gene expression characterisation; NHP;
KW   novel human protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1062
FT                   /*tag=  a
FT                   /product= "G-protein coupled receptor kinase 2"
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PN   WO200168869-A2.
XX
PD   20-SEP-2001.
XX
PF   08-MAR-2001; 2001WO-US007500.
XX
PR   10-MAR-2000; 2000US-0188449P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Walke DW,  Wilganowski NL,  Turner CA;
XX
DR   WPI; 2001-570872/64.
DR   P-PSDB; AAG77816.
XX
PT   New polynucleotides encoding human proteins that share sequence
PT   similarity with animal kinases e.g. G-protein coupled receptor kinases,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Claim 4; Page 32; 34pp; English.
XX
CC   The present cDNA sequence encodes a human G-protein coupled receptor
CC   kinase (GRK), also designated NHP (novel human protein) in the
CC   specification, which is claimed in the invention. The invention comprises
CC   novel human nucleotide and protein sequences which have similarity to G-
CC   protein coupled receptor kinases. Oligonucleotides derived from the
CC   nucleotides of the invention are useful as hybridisation probes for
CC   screening libraries and assessing gene expression patterns. The
CC   nucleotides of the invention are also useful in drug screening and gene
CC   therapy for the modulation of GRK expression. The nucleotides of the
CC   invention can be used to genetically engineer host cells to express GRK
CC   products in vivo. The nucleotide sequences of the invention are also
CC   useful in addressable arrays for identifying and characterising the
CC   temporal and tissue specific expression of a gene and in microarrays to
CC   screen collections of genetic material from patients who have a
CC   particular medical condition. The proteins of the invention are useful
CC   for generating antibodies, as reagents in diagnostic assays, for
CC   identifying other cellular gene products related to GRK, and as reagents
CC   in assays for screening for compounds that are useful in the treatment of
CC   mental, biological or medical disorders/diseases
XX
SQ   Sequence 1062 BP; 237 A; 296 C; 330 G; 199 T; 0 U; 0 Other;

  Query Match             47.6%;  Score 1046.8;  DB 4;  Length 1062;
  Best Local Similarity   99.8%;  Pred. No. 1.9e-260;
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Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
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Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

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Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
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Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGAAAGGT 890
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Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGAAAGGT 600

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Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
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Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

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Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

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Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

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Job time : 598.249 secs
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        Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          August 13, 2004, 10:30:45 ; Search time 5722.66 Seconds
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Scoring table:   IDENTITY_NUC
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Searched:        3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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AX797552
LOCUS       AX797552                2198 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 1 from Patent WO02095032.
ACCESSION   AX797552
VERSION     AX797552.1  GI:37518055
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kapeller-Libermann,R. and Bandaru,R.
  TITLE     Method and compositions of human proteins and uses thereof
  JOURNAL   Patent: WO 02095032-A 1 28-NOV-2002;
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FEATURES                  Location/Qualifiers
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Db          1 GACCCTAAGATGAAGGGACCTCACTATAGGGCTCGAGCGGCCGCCCGGGCAGGTGCTTTC 60

Qy         61 GCCTTGGCAGGTGGAGCATGACCTATCGTGTGCAGTTCCTGGCGGGCTATACATAGCCA 120
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGA 1200

Qy       1201 TGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTC 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 TGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTC 1260

Qy       1261 TGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTG 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 TGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTG 1320

Qy       1321 GCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGG 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 GCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGG 1380

Qy       1381 AAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAA 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 AAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAA 1440

Qy       1441 TGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGA 1500

Qy       1501 AGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 AGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAA 1560

Qy       1561 AAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAA 1620
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Db       1561 AAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAA 1620

Qy       1621 AGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAG 1680
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Db       1621 AGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAG 1680

Qy       1681 CTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCG 1740
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 CTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCG 1740

Qy       1741 CTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGT 1800
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1741 CTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGT 1800

Qy       1801 TCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAA 1860
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1801 TCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAA 1860

Qy       1861 CGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGGGTAATT 1920
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1861 CGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGGGTAATT 1920

Qy       1921 CATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGGCAGCAG 1980
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1921 CATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGGCAGCAG 1980

Qy       1981 GAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAATGAGGGCT 2040
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1981 GAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAATGAGGGCT 2040

Qy       2041 AATCAGTTAGGAGGGACATCACAACCACAAAACAATTCAAAAGACAGGCAAGCTCACTAC 2100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2041 AATCAGTTAGGAGGGACATCACAACCACAAAACAATTCAAAAGACAGGCAAGCTCACTAC 2100

Qy       2101 TAGAACACATTTTATTTTCTTTTTCTTTCTTCATAAAGATGAGTAAAGTCTCAGTTTTCA 2160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2101 TAGAACACATTTTATTTTCTTTTTCTTTCTTCATAAAGATGAGTAAAGTCTCAGTTTTCA 2160

Qy       2161 CTGAGGGCAGGGAAAAGGAACACTCAGGTTTATTTTGA 2198
              ||||||||||||||||||||||||||||||||||||||
Db       2161 CTGAGGGCAGGGAAAAGGAACACTCAGGTTTATTTTGA 2198


RESULT 2
AR225819
LOCUS       AR225819                2249 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6444456.
ACCESSION   AR225819
VERSION     AR225819.1  GI:27263949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2249)
  AUTHORS   Walke,D.W., Wilganowski,N.L. and Turner,C.A. Jr.
  TITLE     Human G-coupled protein receptor kinases and polynucleotides
            encoding the same
  JOURNAL   Patent: US 6444456-A 5 03-SEP-2002;
FEATURES             Location/Qualifiers
     source          1..2249
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             91.4%;  Score 2008.8;  DB 6;  Length 2249;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        175 CAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAG 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 CAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAG 297

Qy        235 CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGG 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGG 357

Qy        295 TGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGC 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGC 417

Qy        355 CCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGC 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 CCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGC 477

Qy        415 TGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGC 474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 TGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGC 537

Qy        475 AGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCA 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCA 597

Qy        535 AGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCA 594
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 AGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCA 657

Qy        595 AAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACC 654
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 AAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACC 717

Qy        655 CGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAG 714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 CGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAG 777

Qy        715 AGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGC 774
              |||||||||||||||||||||||  |||||||||||||||||||||||||||||||||||
Db        778 AGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGC 837

Qy        775 CCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCG 834
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        838 CCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCG 897

Qy        835 AGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTT 894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 AGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTT 957

Qy        895 TTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAAC 954
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        958 TTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAAC 1017

Qy        955 TGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAA 1014
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 TGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAA 1077

Qy       1015 TCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGA 1074
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1078 TCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGA 1137

Qy       1075 CCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACA 1134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 CCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACA 1197

Qy       1135 ACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCT 1194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 ACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCT 1257

Qy       1195 GTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATG 1254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1258 GTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATG 1317

Qy       1255 TGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGA 1314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1318 TGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGA 1377

Qy       1315 AGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCC 1374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1378 AGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCC 1437

Qy       1375 TAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTT 1434
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Db       1438 TAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTT 1497

Qy       1435 ATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGG 1494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1498 ATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGG 1557

Qy       1495 ATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGG 1554
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Db       1558 ATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGG 1617

Qy       1555 AAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCA 1614
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Db       1618 AAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCA 1677

Qy       1615 GAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCC 1674
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Qy       1675 TGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAG 1734
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Db       1738 TGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAG 1797

Qy       1735 ACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATA 1794
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Db       1798 ACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATA 1857

Qy       1795 AGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTA 1854
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1858 AGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTA 1917

Qy       1855 TAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGG 1914
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Db       1918 TAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGG 1977

Qy       1915 GTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGG 1974
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1978 GTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAAATTGCTCTCTTTACCAGACAGG 2037

Qy       1975 CAGCAGGAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAATG 2034
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2038 CAGCAGGAGTCTCGGCTGACATAATCCTCGAATGTTCCACACGTGGAAATCTGTGGAATG 2097

Qy       2035 AGGGCTAATCAGTTAGGAGGGACATCACAACCACAAAACAATTCAAAAGACAGGCAAGCT 2094
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2098 AGGGCTAATCAGTTAGGAGGGACATCACAACCACAAAACAATTCAAAAGACAGGCAAGCT 2157

Qy       2095 CACTACTAGAACACATTTTATTTTCTTTTTCTTTCTTCATAAAGATGAGTAAAGTCTCAG 2154
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2158 CACTACTAGAACACATTTTATTTTCTTTTTCTTTCTTCATAAAGATGAGTAAAGTCTCAG 2217

Qy       2155 TTTTCACTGAGGGCAGGGAAAAGGAACACTCA 2186
              ||||||||||||||||||||||||||||||||
Db       2218 TTTTCACTGAGGGCAGGGAAAAGGAACACTCA 2249


RESULT 3
AX252443
LOCUS       AX252443                2249 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 5 from Patent WO0168869.
ACCESSION   AX252443
VERSION     AX252443.1  GI:15985735
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Walke,D.W., Wilganowski,N.L. and Turner,C.A.
  TITLE     Human g-coupled protein receptor kinases and polynucleotides
            encoding the same
  JOURNAL   Patent: WO 0168869-A 5 20-SEP-2001;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
     source          1..2249
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match             91.4%;  Score 2008.8;  DB 6;  Length 2249;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 2010;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        175 CAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAG 234
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 CAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTCTCACCCGGGAAGGGAAAGCAG 297

Qy        235 CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGG 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 CCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGTGCGCCCCGTGCTCAGCCATGG 357

Qy        295 TGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGC 354
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 TGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGC 417

Qy        355 CCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGC 414
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 CCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGC 477

Qy        415 TGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGC 474
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 TGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGC 537

Qy        475 AGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCA 534
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 AGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCA 597

Qy        535 AGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCA 594
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 AGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCA 657

Qy        595 AAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACC 654
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Db        658 AAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACC 717

Qy        655 CGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAG 714
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        718 CGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAG 777

Qy        715 AGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGC 774
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Db        778 AGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGC 837

Qy        775 CCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCG 834
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Db        838 CCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCG 897

Qy        835 AGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTT 894
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        898 AGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTT 957

Qy        895 TTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAAC 954
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Db        958 TTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAAC 1017

Qy        955 TGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAA 1014
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1018 TGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAA 1077

Qy       1015 TCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGA 1074
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Db       1078 TCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGA 1137

Qy       1075 CCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACA 1134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1138 CCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACA 1197

Qy       1135 ACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCT 1194
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1198 ACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCT 1257

Qy       1195 GTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATG 1254
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1258 GTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATG 1317

Qy       1255 TGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGA 1314
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1318 TGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGA 1377

Qy       1315 AGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCC 1374
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1378 AGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCC 1437

Qy       1375 TAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTT 1434
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Qy       1435 ATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGG 1494
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Qy       1855 TAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAGGAGG 1914
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Qy       2035 AGGGCTAATCAGTTAGGAGGGACATCACAACCACAAAACAATTCAAAAGACAGGCAAGCT 2094
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RESULT 4
AX710216
LOCUS       AX710216                3186 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 4 from Patent WO03018815.
ACCESSION   AX710216
VERSION     AX710216.1  GI:29786804
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Xiao,Y.
  TITLE     Regulation of human g protein-couple receptor kinase
  JOURNAL   Patent: WO 03018815-A 4 06-MAR-2003;
            Bayer Aktiengesellschaft (DE)
FEATURES             Location/Qualifiers
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ORIGIN
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  Query Match             90.5%;  Score 1988.8;  DB 6;  Length 3186;
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Qy        267 TGGGAGTGCGCCCCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGCC 326
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Qy        567 TGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACT 626
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Qy        627 TGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACC 686
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Db        961 GTGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATC 1020

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Qy       1287 TCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGA 1346
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RESULT 5

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ACCESSION   AF282269
VERSION     AF282269.1  GI:17026317
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3186)
  AUTHORS   Weiss,E.R., Ducceschi,M.H., Horner,T.J., Li,A., Craft,C.M. and
            Osawa,S.
  TITLE     Species-specific differences in expression of G-protein-coupled
            receptor kinase (GRK) 7 and GRK1 in mammalian cone photoreceptor
            cells: implications for cone cell phototransduction
  JOURNAL   J. Neurosci. 21 (23), 9175-9184 (2001)
  MEDLINE   21574315
   PUBMED   11717351
REFERENCE   2  (bases 1 to 3186)
  AUTHORS   Osawa,S. and Weiss,E.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Cell Biology and Anatomy, University of
            North Carolina, CB#7090, 108 Taylor Hall, Chapel Hill, NC
            27599-7090, USA
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ORIGIN

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  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1990;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db       1021 GTCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTA 1080

Qy       1287 TCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGA 1346
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Qy       1347 ACCAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTG 1406
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Qy       1407 GACTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAA 1466
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Db       1201 GACTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAA 1260

Qy       1467 GATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTC 1526
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Db       1261 GATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTC 1320

Qy       1527 AAATTCCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCT 1586
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Qy       1647 TTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTG 1706
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Qy       1707 CCAGACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTT 1766
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Qy       1887 CCCAACAGACCTACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTA 1946
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Db       1681 CCCAACAGACCTACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTA 1740

Qy       1947 TTGTAAATTGCTCTCTTTACCAGACAGGCAGCAGGAGTCTCGGCTGACATAATCCTCGAA 2006
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Db       1741 TTGTAAATTGCTCTCTTTACCAGACAGGCAGCAGGAGTCTCGGCTGACATAATCCTCGAA 1800

Qy       2007 TGTTCCACACGTGGAAATCTGTGGAATGAGGGCTAATCAGTTAGGAGGGACATCACAACC 2066
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Db       1861 ACAAAACAATTCAAAAGACAGGCAAGCTCACTACTAGAACACATTTTATTTTCTTTTTCT 1920

Qy       2127 TTCTTCATAAAGATGAGTAAAGTCTCAGTTTTCACTGAGGGCAGGGAAAAGGAACACTCA 2186
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Db       1921 TTCTTCATAAAGATGAGTAAAGTCTCAGTTTTCACTGAGGGCAGGGAAAAGGAACACTCA 1980

Qy       2187 GGTTTATTTTGA 2198
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Db       1981 GGTTTATTTTGA 1992
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RESULT 6
AF439409
LOCUS       AF439409                1799 bp    mRNA    linear   PRI 21-FEB-2002
DEFINITION  Homo sapiens G-protein-coupled receptor kinase 7 (GRK7) mRNA,
            GRK7-S allele, complete cds.
ACCESSION   AF439409
VERSION     AF439409.1  GI:17933258
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1799)
  AUTHORS   Chen,C.K., Zhang,K., Church-Kopish,J., Huang,W., Zhang,H.,
            Chen,Y.J., Frederick,J.M. and Baehr,W.
  TITLE     Characterization of human GRK7 as a potential cone opsin kinase
  JOURNAL   Mol. Vis. 7, 305-313 (2001)
  MEDLINE   21626361
   PUBMED   11754336
REFERENCE   2  (bases 1 to 1799)
  AUTHORS   Baehr,W. and Chen,C.-K.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2001) Ophthalmology, University of Utah, 15
            North/2030 East, Salt Lake City, UT 84112, USA
FEATURES             Location/Qualifiers
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                     /tissue_type="retina"
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                     QPFKDFVTSAFYDKFLQWKLFEMQPVSDKYFTEFRVLGKGGFGEVCAVQVKNTGKMYA
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                     KFHIYNVGTRGLDMSRVIFYSAQIACGMLHLHELGIVYRDMKPENVLLDDLGNCRLSD
                     LGLAVEMKGGKPITQRAGTNGYMAPEILMEKVSYSYPVDWFAMGCSIYEMVAGRTPFK
                     DYKEKVSKEDLKQRTLQDEVKFQHDNFTEEAKDICRLFLAKKPEQRLGSREKSDDPRK
                     HHFFKTINFPRLEAGLIEPPFVPDPSVVYAKDIAEIDDFSEVRGVEFDDKDKQFFKNF
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ORIGIN

  Query Match             81.7%;  Score 1795.8;  DB 9;  Length 1799;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1797;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        154 ACCCTCCACGGGTCCCACCCACAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTC 213
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ACCCTCCACGGGTCCCACCCACAGGCCACAGGACTCACTGTAAATCCCTTGGACGTTGTC 60

Qy        214 TCACCCGGGAAGGGAAAGCAGCCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGT 273
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCACCCGGGAAGGGAAAGCAGCCAGCAGCCCTCCAGCCCTCTTGTGCTTTCCCTGGGAGT 120

Qy        274 GCGCCCCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCG 333
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Db        121 GCGCCCCGTGCTCAGCCATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCG 180

Qy        334 CCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGC 393
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Db        181 CCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGC 240

Qy        394 GTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGA 453
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGA 300

Qy        454 ACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAG 513
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Db        301 ACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAG 360

Qy        514 CCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGC 573
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Db        361 CCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGC 420

Qy        574 TGGCCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGA 633
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Db        421 TGGCCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGA 480

Qy        634 GTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCC 693
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Db        481 GTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCC 540

Qy        694 AAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCA 753
              ||||||||||||||||||||||||||||||||||||||||||||  ||||||||||||||
Db        541 AAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCA 600

Qy        754 TGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGT 813
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGT 660

Qy        814 TTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCA 873
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Db        661 TTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCA 720

Qy        874 GAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGA 933
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Db        721 GAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGA 780

Qy        934 AGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGA 993
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Qy        994 TGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGG 1053
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Db        841 TGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGG 900

Qy       1054 CCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAG 1113
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Db        901 CCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAG 960

Qy       1114 ACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCT 1173
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Db        961 ACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCT 1020

Qy       1174 TTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATC 1233
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Qy       1234 GGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACC 1293
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Db       1081 GGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACC 1140

Qy       1294 TGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATG 1353
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 TGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATG 1200

Qy       1354 GTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGT 1413
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Qy       1414 TTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACA 1473
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Qy       1474 AGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCC 1533
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Db       1321 AGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCC 1380

Qy       1534 AGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAAC 1593
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Qy       1654 AAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACC 1713
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RESULT 7
BD186115
LOCUS       BD186115                1761 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  A novel gene relating to disease and use thereof.
ACCESSION   BD186115
VERSION     BD186115.1  GI:31878315
KEYWORDS    WO 02103020-A/10.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1761)
  AUTHORS   Koyama,N., Tanida,S. and Yamamoto,K.
  TITLE     A novel gene relating to disease and use thereof
  JOURNAL   Patent: WO 02103020-A 10 27-DEC-2002;
            TAKEDA CHEMICAL INDUSTRIES LTD,NOBUYUKI KOYAMA,SEIICHI TANIDA,KOJI
            YAMAMOTO
COMMENT     OS   Homo sapiens (human)
            PN   WO 02103020-A/10
            PD   27-DEC-2002
            PF   14-JUN-2002 WO 2002JP005942
            PR   15-JUN-2001 JP 01P   182654
            PI   NOBUYUKI KOYAMA,SEIICHI TANIDA,KOJI YAMAMOTO
            PC   C12N15/54,C12N9/12,G01N33/50,G01N33/15,C07K16/40,A61K39/395 CC
              A novel gene relating to disease and use thereof FH   Key
                Location/Qualifiers
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             80.0%;  Score 1757.8;  DB 6;  Length 1761;
  Best Local Similarity   99.9%;  Pred. No. 0;
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Qy        326 CAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCG 385
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Qy        386 GCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCT 445
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Qy        506 CTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAA 565
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Qy        566 CTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCAC 625
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Qy        626 TTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCAC 685
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Qy        686 CAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGC 745
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Db        421 CAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGC 480

Qy        746 TGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTA 805
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Db        481 TGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTA 540

Qy        806 CGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCAC 865
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Db        541 CGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCAC 600

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Qy        926 CACTGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGG 985
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Qy        986 CGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGT 1045
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Db        721 CGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGT 780

Qy       1046 CTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAA 1105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAA 840

Qy       1106 TGGGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCG 1165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TGGGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCG 900

Qy       1166 GGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCAT 1225
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCAT 960

Qy       1226 CGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTT 1285
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 CGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTT 1020

Qy       1286 ATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGG 1345
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGG 1080

Qy       1346 AACCAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGT 1405
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Db       1081 AACCAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGT 1140

Qy       1406 GGACTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAA 1465
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Db       1141 GGACTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAA 1200

Qy       1466 AGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGT 1525
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Db       1201 AGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGT 1260

Qy       1526 CAAATTCCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGC 1585
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 CAAATTCCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGC 1320

Qy       1586 TAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAAGTCTGATGATCCCAGGAAACATCA 1645
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 TAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAAGTCTGATGATCCCAGGAAACATCA 1380

Qy       1646 TTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGT 1705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 TTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGT 1440

Qy       1706 GCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGT 1765
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Qy       1766 TCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGC 1825
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Qy       1826 TGTTCCTATAGCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGA 1885
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Qy       1886 CCCCAACAGACCTACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTT 1945
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Db       1621 CCCCAACAGACCTACGGGTTGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTT 1680

Qy       1946 ATTGTAAATTGCTCTCTTTACCAGACAGGCAGCAGGAGTCTCGGCTGACATAATCCTCGA 2005
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1681 ATTGTAAATTGCTCTCTTTACCAGACAGGCAGCAGGAGTCTCGGCTGACATAATCCTCGA 1740

Qy       2006 ATGTTCCACACGTGGAAATCT 2026
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Db       1741 ATGTTCCACACGTGGAAATCT 1761


RESULT 8
AX797554
LOCUS       AX797554                1659 bp    DNA     linear   PAT 04-OCT-2003
DEFINITION  Sequence 3 from Patent WO02095032.
ACCESSION   AX797554
VERSION     AX797554.1  GI:37518056
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kapeller-Libermann,R. and Bandaru,R.
  TITLE     Method and compositions of human proteins and uses thereof
  JOURNAL   Patent: WO 02095032-A 3 28-NOV-2002;
            MILLENIUM PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1..1659
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             75.5%;  Score 1659;  DB 6;  Length 1659;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1659;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
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Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
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Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
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Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
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Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
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Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
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Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

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Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

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Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

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Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
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Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
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Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
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Qy       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
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Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
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Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
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Qy       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
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Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1949
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Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659


RESULT 9
AX642968
LOCUS       AX642968                1662 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 45 from Patent WO01096547.
ACCESSION   AX642968
VERSION     AX642968.1  GI:28550117
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,
            Gandhi,A.R., Tribouley,C.M., Walia,N., Yao,M.G., Lu,D.A.,
            Greenwald,S.R., Ramkumar,J., Griffin,J.A., Kearney,L., Burford,N.,
            Nguyen,D.B., Tang,Y.T., Baughn,M.R., He,A., Thornton,M.,
            Hafalia,A., Patterson,C., Gururajan,R., Lo,T.P., Khan,F.,
            Recipon,S.A., Azimzai,Y., Policky,J.L., Ding,L., Grether,M.,
            Elliott,V.S., Thangavelu,K., Batra,S. and Ison,C.H.
  TITLE     Humain kinases
  JOURNAL   Patent: WO 01096547-A 45 20-DEC-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .1662
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Incyte ID No: 7477204CB1"
ORIGIN

  Query Match             75.5%;  Score 1658.8;  DB 6;  Length 1662;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1660;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
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Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
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Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
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Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
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Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

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Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
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Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
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Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
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Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
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Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
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Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

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Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
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Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

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Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

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Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

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Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662

RESULT 10
AR225817
LOCUS       AR225817                1662 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6444456.
ACCESSION   AR225817
VERSION     AR225817.1  GI:27263947
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1662)
  AUTHORS   Walke,D.W., Wilganowski,N.L. and Turner,C.A. Jr.
  TITLE     Human G-coupled protein receptor kinases and polynucleotides
            encoding the same
  JOURNAL   Patent: US 6444456-A 1 03-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .1662
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             75.5%;  Score 1658.4;  DB 6;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1659;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

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Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

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DEFINITION  Sequence 1 from Patent WO0168869.
ACCESSION   AX252439
VERSION     AX252439.1  GI:15985733
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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REFERENCE   1
  AUTHORS   Walke,D.W., Wilganowski,N.L. and Turner,C.A.
  TITLE     Human g-coupled protein receptor kinases and polynucleotides
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  JOURNAL   Patent: WO 0168869-A 1 20-SEP-2001;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .1662
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ORIGIN

  Query Match            75.5%;  Score 1658.4;  DB 6;  Length 1662;
  Best Local Similarity  99.8%;  Pred. No. 0;
  Matches 1659;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
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DEFINITION  Sequence 1 from patent US 6331423.
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1662)
  AUTHORS   Guegler,K., Beasley,E.M. and Di Francesco,V.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: US 6331423-A 1 18-DEC-2001;
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ORIGIN

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy         1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
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Db          961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy         1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy         1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
                |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db         1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy         1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy         1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy         1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy         1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy         1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy         1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790
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Db         1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy         1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
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Db         1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy         1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
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Qy         1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
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Db         1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662


RESULT 13
AR343544
LOCUS       AR343544                1662 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6579709.
ACCESSION   AR343544
VERSION     AR343544.1  GI:33739257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1662)
  AUTHORS   Guegler,K., Beasley,E.M. and Di Francesco,V.
```

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TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
          human kinase proteins, and uses thereof
JOURNAL   Patent: US 6579709-A 1 17-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .1662
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             75.4%;  Score 1657.2;  DB 6;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1659;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
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Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
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Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
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Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
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Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
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Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
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Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

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Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

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Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

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Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
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Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
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Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
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Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
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Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
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Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
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Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
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Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
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Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
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Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1851 ATTATAGAAACGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
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Db       1561 ATTATAGAAACGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
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Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662


RESULT 14
AX357902
LOCUS       AX357902                1662 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 1 from Patent WO0192496.
ACCESSION   AX357902
VERSION     AX357902.1  GI:18674690
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Guegler,K., di Francesco,V. and Beasley,E.M.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: WO 0192496-A 1 06-DEC-2001;
            Applera Corporation Robert A. Millman Assistant Secretary (US)
FEATURES             Location/Qualifiers
     source          1. .1662
                     /organism="Homo sapiens"
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                      /mol_type="unassigned DNA"
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ORIGIN

  Query Match             75.4%;  Score 1657.2;  DB 6;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1659;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350
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Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470
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Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530
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Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650
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Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770
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Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890
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Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950
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Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010
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Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070
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Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

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Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430
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Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490
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Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550
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Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670
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Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730
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Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

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Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850
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Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910
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Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1952
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Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTGTAA 1662


RESULT 15
AX166511
LOCUS       AX166511                1662 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2 from Patent WO0138503.
ACCESSION   AX166511
VERSION     AX166511.1  GI:14546856
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
            Flanagan,P. and Clary,D.S.
  TITLE     Novel human protein kinases and protein kinase-like enzymes
  JOURNAL   Patent: WO 0138503-A 2 31-MAY-2001;
            Sugen, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches 1658;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

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; Publication No. US20020123464A1
; GENERAL INFORMATION:
;  APPLICANT: KAPELLER-LIBERMANN, Rosana
;  APPLICANT:  BANDARU, Rajasekhar
;  TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Protei
;  TITLE OF INVENTION:  Uses Thereof
;  FILE REFERENCE: 10147-52U1
;  CURRENT APPLICATION NUMBER: US/10/044,205A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: US 60/242,428
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: US 60/241,884
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 60/241,877
;  PRIOR FILING DATE: 2000-10-20
;  NUMBER OF SEQ ID NOS: 44
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US-10-044-205A-3

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Db        1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
               |||||||||||||||||||||||||||||||||||||||
Db        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659


RESULT 2
US-10-044-205A-1
; Sequence 1, Application US/10044205A
; Publication No. US20020123464A1
; GENERAL INFORMATION:
;  APPLICANT: KAPELLER-LIBERMANN, Rosana
;  APPLICANT:  BANDARU, Rajasekhar
;  TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human Proteir
;  TITLE OF INVENTION:  Uses Thereof
;  FILE REFERENCE: 10147-52U1
;  CURRENT APPLICATION NUMBER: US/10/044,205A
;  CURRENT FILING DATE:  2002-04-19
;  PRIOR APPLICATION NUMBER: US 60/242,428
;  PRIOR FILING DATE: 2000-10-23
;  PRIOR APPLICATION NUMBER: US 60/241,884
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: US 60/241,877
;  PRIOR FILING DATE: 2000-10-20
;  NUMBER OF SEQ ID NOS: 44
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 2198
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-044-205A-1

  Query Match             100.0%;  Score 1659;  DB 14;  Length 2198;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1659;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350

Qy          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410

Qy         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1949


RESULT 3
US-10-311-034-45
; Sequence 45, Application US/10311034
; Publication No. US20040023242A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  YUE, Henry
;  APPLICANT:  LAL, Preeti
;  APPLICANT:  BANDMAN, Olga
;  APPLICANT:  BOROWSKY, Mark L.
;  APPLICANT:  AU-YOUNG, Janice
;  APPLICANT:  LU, Yan
;  APPLICANT:  GANDHI, Ameena R.
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  CHAWLA, Narinder K.
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  LU, Dyung Aina M.
;  APPLICANT:  GREENWALD, Sara R.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  GRIFFIN, Jennifer A.
;  APPLICANT:  KEARNEY, Liam
;  APPLICANT:  BURFORD, Neil
;  APPLICANT:  NGUYEN, Danniel B.
;  APPLICANT:  TANG, Y. Tom
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  HE, Ann
;  APPLICANT:  THORNTON, Michael
;  APPLICANT:  HAFALIA, April
;  APPLICANT:  ARVIZU, Chandra S.
;  APPLICANT:  GURURAJAN, Rajagopal
;  APPLICANT:  LO, Terence P.
;  APPLICANT:  KHAH, Farrah A.
;  APPLICANT:  RECIPON, Shirley A.
;  APPLICANT:  AZIMZAI, Yalda
;  APPLICANT:  POLICKY, Jennifer L.
;  APPLICANT:  DING, Li
;  APPLICANT:  GRETHER, Megan
;  APPLICANT:  ELLIOTT, Vicki S.
;  APPLICANT:  THANGAVELU, Kavitha
;  APPLICANT:  BATRA, Sajeev
;  APPLICANT:  ISON, Craig H.
;  TITLE OF INVENTION: HUMAN KINASES
;  FILE REFERENCE: PI-0125 PCT
;  CURRENT APPLICATION NUMBER: US/10/311,034
;  CURRENT FILING DATE:  2002-12-10
;  PRIOR APPLICATION NUMBER: 60/212,073; 60/213,467; 60/215,651; 60/216,605; 60/218,372;
;    60/228,056
;  PRIOR FILING DATE: 2000-06-15; 2000-06-23; 2000-06-30; 2000-07-07; 2000-07-13; 2000-0
;    25
;  NUMBER OF SEQ ID NOS: 52
;  SOFTWARE: PERL Program
; SEQ ID NO 45
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20040023242A1 7477204CB1
US-10-311-034-45

  Query Match             99.8%;  Score 1655.8;  DB 17;  Length 1662;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 4
US-10-451-168-49
; Sequence 49, Application US/10451168
; Publication No. US20040091969A1
; GENERAL INFORMATION:
;  APPLICANT: SMITHKLINE BEECHAM CORPORATION
;  APPLICANT:  SMITHKLINE BEECHAM p.l.c.
;  APPLICANT:  GLAXO GROUP LIMITED
;  TITLE OF INVENTION: NOVEL COMPOUNDS
;  FILE REFERENCE: GP50039
;  CURRENT APPLICATION NUMBER: US/10/451,168
;  CURRENT FILING DATE:  2003-11-12
;  PRIOR APPLICATION NUMBER: PCT/US01/49232
;  PRIOR FILING DATE: 2000-12-17
;  PRIOR APPLICATION NUMBER: 60/256,710
;  PRIOR FILING DATE: 2000-12-19
;  PRIOR APPLICATION NUMBER: 60/257,048
;  PRIOR FILING DATE: 2000-12-20
;  PRIOR APPLICATION NUMBER: 60/260,482
;  PRIOR FILING DATE: 2001-01-09
;  PRIOR APPLICATION NUMBER: 60/264,922
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/266,797
;  PRIOR FILING DATE: 2001-02-06
;  PRIOR APPLICATION NUMBER: 60/276,988
;  PRIOR FILING DATE: 2001-03-19
;  PRIOR APPLICATION NUMBER: 60/281,535
;  PRIOR FILING DATE: 2001-04-04
;  PRIOR APPLICATION NUMBER: 60/289,622
;  PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-451-168-49

  Query Match             99.8%;  Score 1655.8;  DB 17;  Length 1662;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 5
US-10-217-745-5
; Sequence 5, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases an
;  TITLE OF INVENTION:  Polynucleotides
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/10/217,745
;  CURRENT FILING DATE:  2002-08-12
;  PRIOR APPLICATION NUMBER: US/09/802,117
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 2249
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-217-745-5

  Query Match             99.8%;  Score 1655.8;  DB 15;  Length 2249;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 413

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 473

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 533

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 593

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 653

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 713

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 773

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        774 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 833

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 893

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 953

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 1013

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1014 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1073

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1074 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1133

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1134 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1193

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1194 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1253

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1254 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1313

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1373

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1374 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1433

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1434 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1493

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1494 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1553

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1554 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1613

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1614 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1673

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1674 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1733

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1734 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1793

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1794 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1853

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1854 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1913

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1914 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1974 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 2012


RESULT 6
US-10-217-745-1
; Sequence 1, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases an
;  TITLE OF INVENTION:  Polynucleotides
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/10/217,745
;  CURRENT FILING DATE:  2002-08-12
;  PRIOR APPLICATION NUMBER: US/09/802,117
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-217-745-1

  Query Match             99.8%;  Score 1655.4;  DB 15;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1656;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659


RESULT 7
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV
;  CURRENT APPLICATION NUMBER: US/09/964,469
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Human
US-09-964-469-1

  Query Match             99.7%;  Score 1654.2;  DB 9;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1656;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659


RESULT 8
US-10-425-962-1
; Sequence 1, Application US/10425962
; Publication No. US20030180786A1
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV2
;  CURRENT APPLICATION NUMBER: US/10/425,962
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: 09/964,469
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-425-962-1

  Query Match             99.7%;  Score 1654.2;  DB 15;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1656;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659


RESULT 9
US-10-072-012-273
; Sequence 273, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
;  APPLICANT: Tchernev, Velizar
;  APPLICANT:  Spytek, Kimberly
;  APPLICANT:  Zerhusen, Bryan
;  APPLICANT:  Patturajan, Meera
;  APPLICANT:  Shimkets, Richard
;  APPLICANT:  Li, Li
;  APPLICANT:  Gangolli, Esha
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Anderson, David W.
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Miller, Charles E.
;  APPLICANT:  Gerlach, Valerie
;  APPLICANT:  Taupier Jr, Raymond J.
;  APPLICANT:  Gusev, Vladimir Y.
;  APPLICANT:  Colman, Steven D.
;  APPLICANT:  Wolenc, Adam R.
;  APPLICANT:  Pena, Carol E. A
;  APPLICANT:  Furtak, Katarzyna
;  APPLICANT:  Grosse, William M.
;  APPLICANT:  Alsobrook II, John P.
;  APPLICANT:  Lepley, Denise M.
;  APPLICANT:  Rieger, Daniel K.
;  APPLICANT:  Burgess, Catherine E.
;  TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-258
;  CURRENT APPLICATION NUMBER: US/10/072,012
;  CURRENT FILING DATE:  2002-01-31
;  PRIOR APPLICATION NUMBER: 60/265,102
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: 60/265,514
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,517
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,412
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/265,395
;  PRIOR FILING DATE: 2001-01-31
;  PRIOR APPLICATION NUMBER: 60/266,406
;  PRIOR FILING DATE: 2001-02-02
;  PRIOR APPLICATION NUMBER: 60/266,767
;  PRIOR FILING DATE: 2001-02-05
;  PRIOR APPLICATION NUMBER: 60/267,057
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/266,975
;  PRIOR FILING DATE: 2001-02-07
;  PRIOR APPLICATION NUMBER: 60/267,459
;  PRIOR FILING DATE: 2001-02-08
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 1391
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 273
;   LENGTH: 1701
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-072-012-273

  Query Match             95.8%;  Score 1589.8;  DB 13;  Length 1701;
  Best Local Similarity   98.6%;  Pred. No. 0;
  Matches 1642;  Conservative    0;  Mismatches    2;  Indels   21;  Gaps    3;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         19 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 78

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         79 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 138

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        139 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 198

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        199 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 258

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        259 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 318

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 378

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 438

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        439 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 498

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 558

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 618

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660
              |||||||||||||||               ||||||||||||||||||||||||||||||
Db        619 GGTTTTGGGGAGGTA---------------AAAAACACTGGAAGATGTATGCCTGTAAG 663

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        664 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 723

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        724 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 783

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        784 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 843

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        844 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 903

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        904 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 963

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        964 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1023

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAG---GGCTGGAACCAATGGTTACATGGCTCCT 1077
              |||||||||||||||||||||||||||||   ||||||||||||||||||||||||||||
Db       1024 ATGAAGGGTGGCAAGCCCATCACCCAGAGGCAGGCTGGAACCAATGGTTACATGGCTCCT 1083

Qy       1078 GAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGC 1137
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1084 GAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGC 1143

Qy       1138 AGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGT 1197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1144 AGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGT 1203

Qy       1198 AAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTC 1257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1204 AAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTC 1263

Qy       1258 ACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTA 1317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1264 ACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTA 1323

Qy       1318 GGAAGC---AGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAAC 1374
              ||||||   |||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1324 GGAAGCAGGAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAAC 1383

Qy       1375 TTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTT 1434
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1384 TTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTT 1443

Qy       1435 TATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGAT 1494
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1444 TATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGAT 1503

Qy       1495 GACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAG 1554
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1504 GACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAG 1563

Qy       1555 GAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGT 1614
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1564 GAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGT 1623

Qy       1615 TGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1624 TGTGAGGAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1668


RESULT 10
US-10-217-745-3
; Sequence 3, Application US/10217745
; Publication No. US20030004328A1
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. US20030004328A1el Human G-Coupled Protein Receptor Kinases an
;  TITLE OF INVENTION:  Polynucleotides
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/10/217,745
;  CURRENT FILING DATE:  2002-08-12
;  PRIOR APPLICATION NUMBER: US/09/802,117
;  PRIOR FILING DATE: 2001-03-08
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1062
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-217-745-3

  Query Match             63.1%;  Score 1046.8;  DB 15;  Length 1062;
  Best Local Similarity   99.8%;  Pred. No. 3.8e-312;
  Matches 1048;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1050
              ||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1050


RESULT 11
US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. US20020034803A1
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV
;  CURRENT APPLICATION NUMBER: US/09/964,469
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 36651
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(36651)
;   OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

  Query Match             37.2%;  Score 617.4;  DB 9;  Length 36651;
  Best Local Similarity   96.8%;  Pred. No. 1.5e-178;
  Matches  630;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2076 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 2135

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2136 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 2195

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2196 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 2255

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2256 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 2315

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2316 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 2375

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2376 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 2435

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2436 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 2495

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db       2496 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 2555

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2556 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 2615

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2616 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 2675

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTAT 651
              ||||||||||||||| ||| |  ||||  |  |  |     |  || | ||
Db       2676 GGTTTTGGGGAGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCAT 2726


RESULT 12
US-10-425-962-3
; Sequence 3, Application US/10425962
; Publication No. US20030180786A1
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV2
;  CURRENT APPLICATION NUMBER: US/10/425,962
;  CURRENT FILING DATE:  2003-04-30
;  PRIOR APPLICATION NUMBER: 09/964,469
;  PRIOR FILING DATE: 2001-09-28
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 36651
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(36651)
;   OTHER INFORMATION: n = A,T,C or G
US-10-425-962-3

  Query Match             37.2%;  Score 617.4;  DB 15;  Length 36651;
  Best Local Similarity   96.8%;  Pred. No. 1.5e-178;
  Matches  630;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2076 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 2135

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2136 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 2195

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2196 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 2255

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2256 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 2315

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2316 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 2375

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2376 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 2435

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2436 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 2495

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db       2496 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 2555

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2556 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 2615

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2616 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 2675

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTAT 651
              ||||||||||||||| ||| |  ||||  |  |  |     |  || | ||
Db       2676 GGTTTTGGGGAGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCAT 2726


RESULT 13
US-09-851-686-2
; Sequence 2, Application US/09851686
; Patent No. US20020034767A1
; GENERAL INFORMATION:
;  APPLICANT: Benovic, Jeffrey L.
;  APPLICANT:  Gomez, Jorge
;  APPLICANT:  Kunapuli, Priya
;  TITLE OF INVENTION: Compositions and Methods for Modulating the Activity of G Protein-
;  TITLE OF INVENTION:  Receptor Kinases GRK5 and GRK6
;  FILE REFERENCE: JEFF-0118-DIV
;  CURRENT APPLICATION NUMBER: US/09/851,686
;  CURRENT FILING DATE:  2001-10-01
;  PRIOR APPLICATION NUMBER: US 08/464,954
;  PRIOR FILING DATE: 1995-06-06
;  PRIOR APPLICATION NUMBER: US 08/076,084
;  PRIOR FILING DATE: 1993-06-11
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 2848
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-851-686-2
```

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Query Match             25.2%;  Score 418.2;  DB 9;  Length 2848;
Best Local Similarity   56.2%;  Pred. No. 1.1e-117;
Matches  890;  Conservative    0;  Mismatches  683;  Indels   12;  Gaps    5;

Qy           15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74
                ||  || || ||| |  | || ||||| |     ||  |||||||| |       |   |
Db           65 GGAGCTCGAGAACATCGTAGCGAACACGGTACTACTCAAGGCCCGGGAAGGTGGCGGTGG 124

Qy           75 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
                  |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db          125 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 184

Qy          132 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 191
                 ||||  ||||| || |  |  ||    |   |||  ||||||||||| |||| |||  |
Db          185 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACGC 244

Qy          192 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 251
                ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db          245 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 304

Qy          252 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 311
                  ||||||| || |  |||    | |  ||  || ||  ||| |        || |   |
Db          305 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 364

Qy          312 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 371
                 | || ||| |   |   |   | || |  |||   | | |  || |    |   |
Db          365 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 421

Qy          372 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                  ||| | | |||   ||| | | |  |  || ||| ||     | | |     || |
Db          422 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 480

Qy          432 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 491
                  ||            | |  ||||||  ||   |  | | ||   | |   || |||
Db          481 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 538

Qy          492 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
                 || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db          539 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 598

Qy          552 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
                 |||||| |  | ||   |||||   | | | |||| ||||| |||||||| ||||||||
Db          599 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 658

Qy          612 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
                ||| || |||  |||||||     ||| || |||||||||||||| ||||| || || ||
Db          659 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 718

Qy          672 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 731
                 |||||| | ||||||      || |||   ||||| ||    || ||| | ||| ||||
Db          719 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 778

Qy          732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 791
                ||| || | |||    ||  | ||     ||||||| |||| ||||| ||||  |   ||
Db          779 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTATGAGACCAAGGACGCGCT 838

Qy          792 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 851
                 ||||| ||  |||  |||||||| ||||| ||||||||||||||||||||| || ||||
Db          839 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 898

Qy          852 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 911
                |  |  |||| |   |      ||||   |||| ||| | ||| ||||   ||||||  |
Db          899 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 958

Qy          912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 971
                |  | |||| ||        ||||||| ||  ||||| ||||||| |||||  |  | ||
Db          959 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 1018

Qy          972 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
                |||||||| |||| ||  | |  | ||||||||||| || || ||| |  ||   |  ||
Db         1019 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1078

Qy         1032 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1091
                | || ||||||    | | |  || |||   |||||||||||||| |||    |  || |
Db         1079 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1135

Qy         1092 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1151
                 || | | | ||  | |        |||||||  ||  | || |||  | | || || ||
Db         1136 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1195

Qy         1152 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
                | |  | || |   | || ||| |  |    ||| | ||| |||     |||||  || |
Db         1196 GATCACAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1255

Qy         1212 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
                ||          | | | |   |   | |      |       | | |  |||
Db         1256 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGGTTTTCCCCGCAGGCCCGCTC 1315

Qy         1272 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331
                |  |   |    |||| |||      |     | || |  |      |  |  | |  |
Db         1316 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGCCTGGGGTGTCGTGGGGGCAG 1375

Qy         1332 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1391
                  |    ||    | | | || |   ||||||| | | | |||||    || |||| |||
Db         1376 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1435

Qy         1392 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1451
                |||| |  | || || || ||   ||| |||||    |   ||||   ||| ||
Db         1436 TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGGTCT 1495

Qy         1452 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1511
                 || |||||  | ||||||  |||   ||| |||||  | ||    |  ||  |||||||
Db         1496 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGCAGTT 1555

Qy         1512 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1571
                || | || ||||| |||||   ||| || ||  | |||||| | || ||  | || ||
Db         1556 CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1615

Qy         1572 GGGACTGTTTGAGGAACTGAATGAC 1596
                 |     ||  | || ||||||| |
Db         1616 CGAGTGCTTCCAAGAGCTGAATGTC 1640


RESULT 14
US-09-873-367C-142
; Sequence 142, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
;  APPLICANT: Young, Paul
;  APPLICANT:  Soppet, Daniel
;  APPLICANT:  Endress, Gregory
;  APPLICANT:  Augustus, Meena
;  APPLICANT:  Ebner, Reinhard
;  APPLICANT:  Carter, Kenneth
;  TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
;  TITLE OF INVENTION:  Signature Gene Sets
;  FILE REFERENCE: 689290-64
;  CURRENT APPLICATION NUMBER: US/09/873,367C
;  CURRENT FILING DATE:  2003-04-29
;  PRIOR APPLICATION NUMBER: U.S. 60/236,891
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: U.S. 60/236,842
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: U.S. 60/244,867
;  PRIOR FILING DATE: 2000-11-01
;  PRIOR APPLICATION NUMBER: U.S. 60/245,084
;  PRIOR FILING DATE: 2000-11-01
;  NUMBER OF SEQ ID NOS: 1067
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 142
;   LENGTH: 2848
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-873-367C-142
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  Query Match             25.2%;  Score 418.2;  DB 10;  Length 2848;
  Best Local Similarity   56.2%;  Pred. No. 1.1e-117;
  Matches  890;  Conservative    0;  Mismatches  683;  Indels   12;  Gaps    5;

Qy         15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74
              ||  || || ||| |  | || ||||| |     ||  |||||||| |       |   |
Db         65 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 124

Qy         75 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
                |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db        125 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 184

Qy        132 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 191
               ||||  ||||| || |  |  ||    |   |||  ||||||||||| |||| |||  |
Db        185 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACGC 244

Qy        192 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 251
              ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db        245 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 304

Qy        252 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 311
                ||||||| || |  |||    | |  ||  || ||  ||| ||       || |   |
Db        305 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 364

Qy        312 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 371
               | || ||| |   |   |   | || |  |||   | | |  || |    |    |
Db        365 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 421

Qy        372 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                ||| | | |||   ||| | | |  |  || ||| ||     | | |     ||  |
Db        422 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 480

Qy        432 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 491
                ||            | |  ||||||  ||   |  | | ||   | |   || |||
Db        481 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 538

Qy        492 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
               || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db        539 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 598

Qy        552 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
               |||||| |  | ||   ||||||   | | | |||| ||||| |||||||| ||||||||
Db        599 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 658

Qy        612 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
              ||| || |||  |||||||     ||| || |||||||||||||| ||||| || || ||
Db        659 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 718

Qy        672 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 731
               |||||| | ||||||      || |||   ||||| ||    || ||| | ||| ||||
Db        719 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 778

Qy        732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 791
              ||| || | |||    ||  | ||     ||||||| |||| ||||| ||||  |   ||
Db        779 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTATGAGACCAAGGACGCGCT 838

Qy        792 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 851
               ||||| ||  |||  |||||||| ||||| ||||||||||||||||||||| || ||||
Db        839 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 898

Qy        852 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 911
              |  |  |||| |   |      ||||   |||| ||| | ||| ||||   ||||||  |
Db        899 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 958

Qy        912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 971
              |  | |||| ||        ||||||| ||  ||||| ||||||| |||||  |  | ||
Db        959 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 1018

Qy        972 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
              |||||||| |||| ||  | |  | ||||||||||| || || ||| |  ||   |  ||
Db       1019 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1078

Qy       1032 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1091
              | || ||||||    | | |  || |||   |||||||||||||| |||    |  || |
Db       1079 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1135

Qy       1092 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1151
               || | | | ||  | |        |||||||  ||  | || |||  | | || || ||
Db       1136 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1195

Qy       1152 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
              | | || || |   | || ||| |  |    ||| | ||| |||     |||||  || |
Db       1196 GATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1255

Qy       1212 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
              ||          | | | |   |   | |      |       | | |  |||
Db       1256 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGCTTTTCCCCGCAGGCCCGCTC 1315

Qy       1272 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331
              |  |   |    |||| |||      |     | || |  |      |  |  | |  |
Db       1316 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGCCTGGGGTGTCGTGGGGGCAG 1375

Qy       1332 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1391
                |    ||    | ||  || |   ||||||| | | | |||||    || |||| |||
Db       1376 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1435

Qy       1392 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1451
              |||| |  | || || || ||   ||| ||||||    |   ||||   ||| ||  |
Db       1436 TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGTTCT 1495

Qy       1452 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1511
               || |||||  | ||||||  |||   ||| |||||  | ||    |  ||  || | ||
Db       1496 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGGACTT 1555

Qy       1512 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1571
              || | | || ||||| |||||   ||| || ||  | |||||| | || ||  | || ||
Db       1556 CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1615

Qy       1572 GGGACTGTTTGAGGAACTGAATGAC 1596
               |     ||  | || ||||||| |
Db       1616 CGAGTGCTTCCAAGAGCTGAATGTC 1640


RESULT 15
US-10-159-856-4
; Sequence 4, Application US/10159856
; Publication No. US20030228689A1
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF G PROTEIN-COUPLED RECEPTOR KINASE 6 EXPRES
;  FILE REFERENCE: RTS-0365
;  CURRENT APPLICATION NUMBER: US/10/159,856
;  CURRENT FILING DATE:  2002-05-31
;  NUMBER OF SEQ ID NOS: 134
; SEQ ID NO 4
;   LENGTH: 2848
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (63)...(1793)
US-10-159-856-4

  Query Match             25.2%;  Score 418.2;  DB 16;  Length 2848;
  Best Local Similarity   56.2%;  Pred. No. 1.1e-117;
  Matches  890;  Conservative    0;  Mismatches  683;  Indels   12;  Gaps    5;

Qy         15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74
              ||  || || ||| |  | || ||||| |     ||  |||||||| |       |   |
Db         65 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 124

Qy         75 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
                |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db        125 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 184
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Qy        132 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 191
               ||||  |||||| || |  |  ||    |   |||  ||||||||||| |||| |||  |
Db        185 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACGC 244

Qy        192 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 251
              ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db        245 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 304

Qy        252 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 311
                ||||||| || |  |||    | |  ||  || ||  ||| |        || |   |
Db        305 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 364

Qy        312 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 371
               | || ||| |   |   |   | || |  |||   | | |  || |    |   |
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Qy        372 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
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Db        422 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 480

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Db        481 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 538

Qy        492 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
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Qy        552 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
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Qy        612 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
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Qy        672 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 731
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Qy        732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 791
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Qy        912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 971
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Qy        972 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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    20   1208.6     72.9   3095 10 AF063016                     AF063016 Spermophi
    21   1187.8     71.6   1191  6 BD186106                    BD186106 A novel g .
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                               ALIGNMENTS

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DEFINITION  Sequence 3 from Patent WO02095032.
ACCESSION   AX797554
VERSION     AX797554.1  GI:37518056
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kapeller-Libermann,R. and Bandaru,R.
  TITLE     Method and compositions of human proteins and uses thereof
  JOURNAL   Patent: WO 02095032-A 3 28-NOV-2002;
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ORIGIN

  Query Match             100.0%;  Score 1659;  DB 6;  Length 1659;
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RESULT 2
AX797552
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DEFINITION  Sequence 1 from Patent WO02095032.
ACCESSION   AX797552
VERSION     AX797552.1  GI:37518055
KEYWORDS    .
SOURCE      Homo sapiens (human)
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kapeller-Libermann,R. and Bandaru,R.
  TITLE     Method and compositions of human proteins and uses thereof
  JOURNAL   Patent: WO 02095032-A 1 28-NOV-2002;
            MILLENIUM PHARMACEUTICALS, INC. (US)
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Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
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Db        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
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Db        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
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Db        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710

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Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
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Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
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Db        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
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Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
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Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
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Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
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Db       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
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Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1949


RESULT 3
AX642968
LOCUS       AX642968                1662 bp    DNA     linear   PAT 24-FEB-2003
DEFINITION  Sequence 45 from Patent WO01096547.
ACCESSION   AX642968
VERSION     AX642968.1  GI:28550117
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Yue,H., Lal,P., Bandman,O., Borowsky,M., Au-Young,J., Lu,Y.,
            Gandhi,A.R., Tribouley,C.M., Walia,N., Yao,M.G., Lu,D.A.,
            Greenwald,S.R., Ramkumar,J., Griffin,J.A., Kearney,L., Burford,N.,
            Nguyen,D.B., Tang,Y.T., Baughn,M.R., He,A., Thornton,M.,
            Hafalia,A., Patterson,C., Gururajan,R., Lo,T.P., Khan,F.,
            Recipon,S.A., Azimzai,Y., Policky,J.L., Ding,L., Grether,M.,
            Elliott,V.S., Thangavelu,K., Batra,S. and Ison,C.H.
  TITLE     Humain kinases
  JOURNAL   Patent: WO 01096547-A 45 20-DEC-2001;
            Incyte Genomics, Inc. (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /note="Incyte ID No: 7477204CB1"
ORIGIN

  Query Match             99.8%;  Score 1655.8;  DB 6;  Length 1662;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
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Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

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Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
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Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

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Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660

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Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
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Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

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Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
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RESULT 4
BD186115
LOCUS       BD186115                1761 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  A novel gene relating to disease and use thereof.
ACCESSION   BD186115
VERSION     BD186115.1  GI:31878315
KEYWORDS    WO 02103020-A/10.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1761)
  AUTHORS   Koyama,N., Tanida,S. and Yamamoto,K.
  TITLE     A novel gene relating to disease and use thereof
  JOURNAL   Patent: WO 02103020-A 10 27-DEC-2002;
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            YAMAMOTO
COMMENT     OS   Homo sapiens (human)
            PN   WO 02103020-A/10
            PD   27-DEC-2002
            PF   14-JUN-2002 WO 2002JP005942
            PR   15-JUN-2001 JP 01P   182654
            PI   NOBUYUKI KOYAMA,SEIICHI TANIDA,KOJI YAMAMOTO
            PC   C12N15/54,C12N9/12,G01N33/50,G01N33/15,C07K16/40,A61K39/395 CC
              A novel gene relating to disease and use thereof FH    Key
                Location/Qualifiers
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FEATURES             Location/Qualifiers
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ORIGIN

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Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
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Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
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Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
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Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
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Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
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RESULT 5
AF439409
LOCUS       AF439409                1799 bp    mRNA    linear   PRI 21-FEB-2002
DEFINITION  Homo sapiens G-protein-coupled receptor kinase 7 (GRK7) mRNA,
            GRK7-S allele, complete cds.
ACCESSION   AF439409
VERSION     AF439409.1  GI:17933258
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1799)
  AUTHORS   Chen,C.K., Zhang,K., Church-Kopish,J., Huang,W., Zhang,H.,
            Chen,Y.J., Frederick,J.M. and Baehr,W.
  TITLE     Characterization of human GRK7 as a potential cone opsin kinase
  JOURNAL   Mol. Vis. 7, 305-313 (2001)
  MEDLINE   21626361
   PUBMED   11754336
REFERENCE   2  (bases 1 to 1799)
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AUTHORS   Baehr,W. and Chen,C.-K.
TITLE     Direct Submission
JOURNAL   Submitted (23-OCT-2001) Ophthalmology, University of Utah, 15
          North/2030 East, Salt Lake City, UT 84112, USA
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ORIGIN

  Query Match             99.8%;  Score 1655.8;  DB 9;  Length 1799;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
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Db        138 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 197

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
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Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
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Db        258 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 317

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
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Db        378 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 437

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Db        438 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 497

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Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
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Db        558 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 617

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
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Db        738 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 797

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Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
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Db        978 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1037

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
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Db       1158 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1217

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
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Db       1278 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1337

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Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
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RESULT 6
AR225819
LOCUS       AR225819                2249 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 5 from patent US 6444456.
ACCESSION   AR225819
VERSION     AR225819.1  GI:27263949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2249)
  AUTHORS   Walke,D.W., Wilganowski,N.L. and Turner,C.A. Jr.
  TITLE     Human G-coupled protein receptor kinases and polynucleotides
            encoding the same
  JOURNAL   Patent: US 6444456-A 5 03-SEP-2002;
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ORIGIN

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Db      474 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 533

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Qy      301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
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Db      654 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 713

Qy      361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
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Db      834 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 893

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Db     1134 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1193

Qy      841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
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Qy      961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
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Qy     1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
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Db     1794 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1853

Qy     1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
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Db     1854 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1913

Qy     1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
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Db     1914 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973

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Db     1974 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 2012

RESULT 7
AX252443
LOCUS       AX252443                2249 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 5 from Patent WO0168869.
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ACCESSION   AX252443
VERSION     AX252443.1  GI:15985735
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Walke,D.W., Wilganowski,N.L. and Turner,C.A.
  TITLE     Human g-coupled protein receptor kinases and polynucleotides
            encoding the same
  JOURNAL   Patent: WO 0168869-A 5 20-SEP-2001;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
     source          1. .2249
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ORIGIN

  Query Match             99.8%;  Score 1655.8;  DB 6;  Length 2249;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy            1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
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Db          354 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 413

Qy           61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
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Db          414 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 473

Qy          121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
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Db          474 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 533

Qy          181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
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Qy          241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
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Qy          481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
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Qy          961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
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Db         1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1373

Qy         1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
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Qy         1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
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Db         1914 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973

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Db         1974 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 2012


RESULT 8
AX710216
LOCUS       AX710216                3186 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 4 from Patent WO03018815.
ACCESSION   AX710216
VERSION     AX710216.1  GI:29786804
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE       1
  AUTHORS       Xiao,Y.
  TITLE         Regulation of human g protein-couple receptor kinase
  JOURNAL       Patent: WO 03018815-A 4 06-MAR-2003;
                Bayer Aktiengesellschaft (DE)
FEATURES                 Location/Qualifiers
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ORIGIN

  Query Match             99.8%;  Score 1655.8;  DB 6;  Length 3186;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db        445 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 504

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
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Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
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Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
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RESULT 9
AF282269
LOCUS       AF282269                3186 bp    mRNA    linear   PRI 21-NOV-2001
DEFINITION  Homo sapiens G protein-coupled receptor kinase 7 mRNA, complete
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ACCESSION   AF282269
VERSION     AF282269.1  GI:17026317
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3186)
  AUTHORS   Weiss,E.R., Ducceschi,M.H., Horner,T.J., Li,A., Craft,C.M. and
            Osawa,S.
  TITLE     Species-specific differences in expression of G-protein-coupled
            receptor kinase (GRK) 7 and GRK1 in mammalian cone photoreceptor
            cells: implications for cone cell phototransduction
  JOURNAL   J. Neurosci. 21 (23), 9175-9184 (2001)
  MEDLINE   21574315
   PUBMED   11717351
REFERENCE   2  (bases 1 to 3186)
  AUTHORS   Osawa,S. and Weiss,E.R.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUN-2000) Cell Biology and Anatomy, University of
            North Carolina, CB#7090, 108 Taylor Hall, Chapel Hill, NC
            27599-7090, USA
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ORIGIN

  Query Match             99.8%;  Score 1655.8;  DB 9;  Length 3186;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
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Db        145 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 204

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
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Db        205 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 264

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 324

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
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Db        325 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 384

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
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Db        385 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 444

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
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Db        445 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 504

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
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Db        505 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 564

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 624

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
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Db        625 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 684

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
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Db        685 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 744

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
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Db        745 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 804

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
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Db        805 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 864

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
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Db        865 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 924

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
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Db        925 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 984

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1044

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
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Db       1045 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1104

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
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Db       1105 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1164

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
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Db       1165 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1224

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
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Db       1225 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1284

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1285 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1344

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1345 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1404

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
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Db       1405 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1464

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
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Db       1465 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1524

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1525 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1584

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1585 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1644

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1645 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1704

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
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Db       1705 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1743

RESULT 10
AR225817
LOCUS       AR225817                1662 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6444456.
ACCESSION   AR225817
VERSION     AR225817.1  GI:27263947
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1662)
  AUTHORS   Walke,D.W., Wilganowski,N.L. and Turner,C.A. Jr.
  TITLE     Human G-coupled protein receptor kinases and polynucleotides
            encoding the same
  JOURNAL   Patent: US 6444456-A 1 03-SEP-2002;
FEATURES             Location/Qualifiers
     source          1. .1662
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.8%;  Score 1655.4;  DB 6;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1656;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
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Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

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Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
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Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
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Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
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Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
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Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

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Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

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Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
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Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

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Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
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Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
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Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

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Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
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Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
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Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
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Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
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RESULT 11
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AX252439
LOCUS       AX252439                1662 bp    DNA     linear   PAT 05-OCT-2001
DEFINITION  Sequence 1 from Patent WO0168869.
ACCESSION   AX252439
VERSION     AX252439.1  GI:15985733
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Walke,D.W., Wilganowski,N.L. and Turner,C.A.
  TITLE     Human g-coupled protein receptor kinases and polynucleotides
            encoding the same
  JOURNAL   Patent: WO 0168869-A 1 20-SEP-2001;
            Lexicon Genetics Incorporated (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             99.8%;  Score 1655.4;  DB 6;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
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Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
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Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
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Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
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Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
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Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
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Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
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Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
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Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy.       541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
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Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
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Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
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Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

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Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

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Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
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Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
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Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
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Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
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Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 12
AR263766
LOCUS       AR263766                1662 bp    DNA     linear   PAT 29-JAN-2003
DEFINITION  Sequence 1 from patent US 6331423.
ACCESSION   AR263766
VERSION     AR263766.1  GI:28075747
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KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1662)
  AUTHORS   Guegler,K., Beasley,E.M. and Di Francesco,V.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: US 6331423-A 1 18-DEC-2001;
FEATURES             Location/Qualifiers
     source          1..1662
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.7%;  Score 1654.2;  DB 6;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1656;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
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Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
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Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
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Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
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Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 13
AR343544
LOCUS       AR343544                1662 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 1 from patent US 6579709.
ACCESSION   AR343544
VERSION     AR343544.1  GI:33739257
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1662)
  AUTHORS   Guegler,K., Beasley,E.M. and Di Francesco,V.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: US 6579709-A 1 17-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .1662
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             99.7%;  Score 1654.2;  DB 6;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1656;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
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Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
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Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
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Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
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Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
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Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
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Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659


RESULT 14
AX357902
LOCUS       AX357902                1662 bp    DNA     linear   PAT 13-FEB-2002
DEFINITION  Sequence 1 from Patent WO0192496.
ACCESSION   AX357902
VERSION     AX357902.1  GI:18674690
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Guegler,K., di Francesco,V. and Beasley,E.M.
  TITLE     Isolated human kinase proteins, nucleic acid molecules encoding
            human kinase proteins, and uses thereof
  JOURNAL   Patent: WO 0192496-A 1 06-DEC-2001;
            Applera Corporation Robert A. Millman Assistant Secretary (US)
FEATURES             Location/Qualifiers
     source          1. .1662
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
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ORIGIN

  Query Match             99.7%;  Score 1654.2;  DB 6;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1656;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
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Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
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Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
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Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
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Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
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RESULT 15
AX166511
LOCUS       AX166511                1662 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 2 from Patent WO0138503.
ACCESSION   AX166511
VERSION     AX166511.1  GI:14546856
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,
            Flanagan,P. and Clary,D.S.
  TITLE     Novel human protein kinases and protein kinase-like enzymes
  JOURNAL   Patent: WO 0138503-A 2 31-MAY-2001;
            Sugen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1..1662
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             99.6%;  Score 1652.6;  DB 6;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1655;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;
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Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
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Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
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Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
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Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
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Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
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Db        961 AATGGGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

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OM nucleic - nucleic search, using sw model

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                            ALIGNMENTS

RESULT 1
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ID   ABS57375 standard; cDNA; 2198 BP.
XX
AC   ABS57375;
XX
DT   04-FEB-2003  (first entry)
XX
DE   cDNA encoding human GPCR kinase (GPCRK) 69087.
XX
KW   Human; G protein coupled receptor kinase; GPCRK 69087;
KW   cellular proliferative disorder; differentiative disorder;
KW   haematopoietic neoplastic disorder; leukaemia; carcinoma; sarcoma;
KW   metastatic disorder; cytostatic; gene therapy; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /note= "The coding sequence given as SEQ ID No:3 is
FT                   specifically claimed in Claim 1"
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PD   05-SEP-2002.
XX
PF   22-OCT-2001; 2001US-00044205.
XX
PR   19-OCT-2000; 2000US-0241884P.
PR   20-OCT-2000; 2000US-0241877P.
PR   23-OCT-2000; 2000US-0242428P.
XX
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Kapeller-Libermann R,  Bandaru R;
XX
DR   WPI; 2003-066811/06.
DR   P-PSDB; ABG72173.
XX
PT   Novel isolated G protein coupled receptor kinase, 69087, nuclear
PT   signaling protein, 15821 or mitogen activated protein kinase phosphatase,
PT   15418, useful for treating cellular proliferative or differentiative
PT   disorders.
XX
```

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PS   Claim 1; Fig 1; 98pp; English.
XX
CC   The present invention relates to the isolation of a novel human G protein
CC   coupled receptor (GPCR) kinase (GPCRK) designated 69087), a novel human
CC   nuclear signalling protein designated 15821, and a novel human mitogen-
CC   activated protein kinase (MAPK) phosphatase MAPKP designated 15418, and
CC   the polynucleotide sequences encoding them. The sequences of the
CC   invention are useful for treating and diagnosing disorders such as
CC   cellular proliferative and differentiative disorders (e.g. haematopoietic
CC   neoplastic disorders, leukaemia, carcinoma, sarcoma or metastatic
CC   disorders). They are also useful in screening assays, detection assays
CC   (e.g. chromosomal mapping, tissue typing, forensic biology), predictive
CC   medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical
CC   trials and pharmacogenomics), and in methods of treatment (e.g.
CC   therapeutic and prophylactic). The sequences may also be used to screen
CC   public databases to identify other family members or related sequences.
CC   The polypeptide sequences are useful as immunogens to generate antibodies
CC   that bind the polypeptides. The polynucleotide sequences are useful for
CC   mapping their respective genes on a chromosome, identifying gene regions
CC   associated with cellular proliferative or differentiative disorders, and
CC   in gene therapy. The present sequence encodes human GPCRK 69087
XX
SQ   Sequence 2198 BP; 558 A; 557 C; 607 G; 476 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 1659;  DB 7;  Length 2198;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches 1659;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 350

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 410

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 470

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 530

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 590

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 650

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        651 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 710

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        711 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 770

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        771 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 830

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        831 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 890

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        891 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 950

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        951 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1010

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1011 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1070

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1071 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1130

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1131 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1190

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1191 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1250

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1251 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1310

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1311 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1370

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1371 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1430

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1431 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1490

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1491 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1550

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1551 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1610

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1611 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1670

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1671 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1730

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1731 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1790

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1791 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1850

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1851 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1910

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1911 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1949


RESULT 2
ABQ86178
ID   ABQ86178 standard; DNA; 1662 BP.
XX
AC   ABQ86178;
```

```
XX
DT   10-SEP-2002  (first entry)
XX
DE   Novel human gene. SEQ ID 49.
XX
KW   Human; cytostatic; vulnerary; antiarteriosclerotic; antiparkinsonian;
KW   nootropic; neuroprotective; immunosuppressive; haemostatic;
KW   antiinflammatory; cardiant; antiulcer; virucide; antithyroid;
KW   cerebroprotective; anorectic; metabolic; vaccine; cancer; infection;
KW   wound healing disorders; atherosclerosis; Parkinson's disease;
KW   Alzheimer's disease; autoimmune disorder; haematopoietic disorder;
KW   inflammation; neoplastic disease; nervous system disorder;
KW   cardiovascular disorders; pancreatitis; respiratory disorder;
KW   hyperproliferation; systemic autoimmune disease; hyper-immunity;
KW   developmental abnormality; gastrointestinal ulceration; neuropathy;
KW   haematological disease; metabolic disease; sperm dysfunction;
KW   thyroid disorder; hypothyroidism; brain damage; colitis;
KW   cone photo- transduction deficiency; neurological disease; stroke;
KW   angiogenesis; ovulation disorder; spinal cord; thyroid gland; heart;
KW   trachea; thymus; lymph node; muscular system; obesity; anorexia;
KW   growth abnormality; precocious puberty; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200250105-A1.
XX
PD   27-JUN-2002.
XX
PF   17-DEC-2001; 2001WO-US049232.
XX
PR   19-DEC-2000; 2000US-0256710P.
PR   20-DEC-2000; 2000US-0257048P.
PR   09-JAN-2001; 2001US-0260482P.
PR   30-JAN-2001; 2001US-0264922P.
PR   06-FEB-2001; 2001US-0266797P.
PR   19-MAR-2001; 2001US-0276988P.
PR   04-APR-2001; 2001US-0281535P.
PR   08-MAY-2001; 2001US-0289622P.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
PA   (SMIK ) SMITHKLINE BEECHAM PLC.
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Agarwal P,  Birkeland M,  Cogswell JP,  Kabnick KF,  Lai Y;
PI   Martensen SA,  Rizvi SK,  Smith RF,  Strum JC,  Xie Q;
XX
DR   WPI; 2002-508784/54.
DR   P-PSDB; ABP61013.
XX
PT   Secreted proteins and polynucleotides useful as vaccines for preventing
PT   or treating various diseases e.g. cancer, wounds, atherosclerosis,
PT   Parkinson's disease, Alzheimer's disease, infection, autoimmune disorder.
XX
PS   Claim 2(a); Page 255-256; 335pp; English.
XX
CC   The invention relates to an isolated polypeptide with signal sequences
CC   which allow it to be secreted extracellularly or membrane associated. The
CC   activity of polypeptides of the invention may be described as,
CC   cytostatic, vulnerary, antiarteriosclerotic, antiparkinsonian, nootropic,
CC   neuroprotective, immunosuppressive, haemostatic, antiinflammatory,
CC   cardiant, antiulcer, virucide, antithyroid, cerebroprotective, anorectic,
CC   and metabolic. Polypeptides and polynucleotides of the invention are
CC   useful in the treatment, or as a vaccine in the prevention of, cancer,
CC   wound healing disorders, infection, atherosclerosis, Parkinson's disease
CC   and Alzheimer's disease, autoimmune disorder, haematopoietic disorder,
CC   inflammation, neoplastic diseases, nervous system related disorders and
CC   cardiovascular disorders, pancreatitis, respiratory disorder,
CC   hyperproliferation, systemic autoimmune disease, hyper-immunity,
CC   developmental abnormality, gastrointestinal ulceration, neuropathy,
CC   haematological diseases, metabolic diseases, sperm dysfunction, thyroid
CC   disorders e.g. hypothyroidism, brain damages, colitis, cone photo-
CC   transduction deficiency, neurological diseases, stroke, angiogenesis,
CC   ovulation disorders, diseases in the spinal cord, thyroid gland, heart,
CC   trachea, thymus, lymph node and muscular system, obesity, anorexia,
CC   growth abnormalities, and alleviation of precocious puberty. The
CC   sequences given in records ABQ86130-ABQ86184 represent novel human cDNA's
CC   of the invention
XX
SQ   Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 1655.8;  DB 6;  Length 1662;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
               |||||||||||||||||||||||||||||||||||||||
Db        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659


RESULT 3
AAD26466
ID   AAD26466 standard; cDNA; 1662 BP.
XX
AC   AAD26466;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Human kinase PKIN-19 cDNA.
XX
KW   Human; kinase; PKIN-19; cancer; leukaemia; adenocarcinoma; osteoporosis;
KW   immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease;
KW   Acquired Immune Deficiency Syndrome; AIDS; Addison's disease; anaemia;
KW   allergy; asthma; adult respiratory distress syndrome; multiple sclerosis;
KW   autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis;
KW   Good pasture's syndrome; Graves' disease; pancreatitis; psoriasis;
KW   rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome;
KW   hepatitis; hypothyroidism; cerebral palsy; cataract; angina pectoris;
KW   cardiovascular disease; hypertension; vasculitis; myocarditis; obesity;
KW   congestive heart failure; ischaemic heart disease; lung tumour; gout;
KW   fatty liver; Niemann-Pick's disease; gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "Human PKIN-19 protein"
XX
PN   WO200196547-A2.
XX
PD   20-DEC-2001.
XX
PF   14-JUN-2001; 2001WO-US019444.
XX
PR   15-JUN-2000; 2000US-0212073P.
PR   23-JUN-2000; 2000US-0213467P.
PR   30-JUN-2000; 2000US-0215651P.
PR   07-JUL-2000; 2000US-0216605P.
PR   13-JUL-2000; 2000US-0218372P.
PR   25-AUG-2000; 2000US-0228056P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Yue H,  Lal P,  Bandman O,  Borowsky ML,  Au-Young J,  Lu Y;
PI   Gandhi AR,  Tribouley CM,  Walia NK,  Yao MG,  Lu DAM,  Greenwald SR;
PI   Ramkumar J,  Griffin JA,  Kearney L,  Burford N,  Nguyen DB,  Tang YT;
PI   Baughn MR,  He A,  Thornton M,  Hafalia A,  Patterson C,  Gururajan R;
PI   Lo TP,  Khan F,  Recipon SA,  Azimzai Y,  Policky JL,  Ding L;
PI   Grether M,  Elliott VS,  Thangavelu K,  Batra S,  Ison CH;
XX
DR   WPI; 2002-090207/12.
DR   P-PSDB; AAE16273.
XX
PT   New polypeptides, useful for diagnosing, treating or preventing disorders
PT   of growth and development, cardiovascular and lipid, and diseases such as
PT   cancer, comprise human kinase polypeptides.
XX
PS   Claim 5; Page 190; 197pp; English.
XX
CC   The invention relates to human kinase PKIN proteins and their
CC   corresponding cDNAs. A composition containing PKIN agonist is useful for
CC   treating a disease or condition associated with decreased expression of
CC   PKIN and a composition comprising PKIN antagonist is useful for treating
CC   a disease or condition associated with overexpression of PKIN. The
CC   disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma,
CC   myeloma, sarcoma, teratocarcinoma, Hodgkin's disease); immune disorder
CC   (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease,
CC   atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,
CC   autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes
CC   mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease,
CC   osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,
CC   rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis,
CC   bacterial, parasitic, fungal, viral, protozoal and helminthic infections)
CC   growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,
CC   Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
CC   vascular disease (arteriovenous fistula, hypertension, vasculitis,
CC   aneurysms, congestive heart failure, angina pectoris, myocarditis,
CC   ischaemic heart disease, chronic bronchitis, lung tumours); lipid
CC   disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,
CC   hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity
CC   of a test compound and in gene therapy. The present sequence is human
CC   PKIN-19 cDNA
XX
SQ   Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 1655.8;  DB 6;  Length 1662;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
```

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               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy         361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy         421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
               |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db         421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660

Qy         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy        1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy        1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy        1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy        1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy        1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
               |||||||||||||||||||||||||||||||||||||||
Db        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
```

```
RESULT 4
AAD46350
ID   AAD46350 standard; cDNA; 1662 BP.
XX
AC   AAD46350;
XX
DT   27-JAN-2003  (first entry)
XX
DE   Human cone opsin kinase (GRK7) cDNA.
XX
KW   Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
KW   GRK7; cone visual signalling; visual sensitivity; visual resolution;
KW   night blindness; colour blindness; Oguchi disease; Pineal gland activity;
KW   chronobiological desynchrony; depression; anxiety; memory loss; headache;
KW   mental fogginess; fatigue; jet lag; circadian rhythm; ophthalmological;
KW   gene therapy; antidepressant; analgesic; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "Human GRK7 protein"
XX
PN   WO200272541-A2.
XX
PD   19-SEP-2002.
XX
PF   07-MAR-2002; 2002WO-US007025.
XX
PR   07-MAR-2001; 2001US-0274006P.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Bird TA,  Spencer M,  Mosley BA;
XX
DR   WPI; 2002-723307/78.
DR   P-PSDB; AAE28952.
```

```
XX
PT   Identifying compounds that alter inhibition of cone opsin kinase
PT   polypeptide activity for treating a conditions related to cone visual
PT   signaling, comprises mixing a compound with a cone opsin kinase and with
PT   an inhibitory polypeptide.
XX
PS   Example 4; Page 45-46; 61pp; English.
XX
CC   The present invention relates to novel human cone opsin kinase (G-protein
CC   coupled receptor kinase 7; GRK7) and their corresponding polynucleotides.
CC   The invention further relates to a method of identifying compounds that
CC   alter the inhibition of GRK7 polypeptide activity which involves mixing a
CC   test compound with GRK7 protein and an inhibitory polypeptide and
CC   determining if the test compound alters the inhibition of GRK7 protein
CC   activity by the inhibitory polypeptide. GRk7 sequences are useful for
CC   treating conditions related to cone visual signalling (e.g., night
CC   blindness, colour blindness, difficulty with colour vision, visual
CC   sensitivity, visual resolution or in adapting to changes in light
CC   intensity, Oguchi disease or dominant congenital stationary night
CC   blindness), Pineal gland activity (e.g., chronobiological desynchrony,
CC   depression, anxiety, mental fogginess, memory loss, headaches, fatigue,
CC   or jet lag). Agonists of GRK7 polypeptide activity may be used to treat
CC   or ameliorate symptoms of a disease for which increased GRK7 polypeptide
CC   activity is beneficial, e.g., decreased colour sensitivity or other cone
CC   photoreceptor-mediated diseases. The GRK7 proteins are also useful in the
CC   preparation of a medicament for treating a condition or disease related
CC   to cone photoreceptor visual signaling or circadian rhythm, as molecular
CC   probes to screen for inherited defects in colour vision, circadian rhythm
CC   and vision resolution. They are also used as gene therapy tools for
CC   individuals with such disorders. The present sequence is human GRK7 cDNA
XX
SQ   Sequence 1662 BP; 420 A; 411 C; 479 G; 352 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 1655.8;  DB 6;  Length 1662;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
```

```
                 |||||||||||||||||||||||||||||||||||||||
Db         1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659

RESULT 5
ABZ56943
ID   ABZ56943 standard; DNA; 1761 BP.
XX
AC   ABZ56943;
XX
DT   04-APR-2003  (first entry)
XX
DE   Human gene sequence relative to the invention # SEQ ID 11.
XX
KW   Human; heart disease; cancer; omentopathy; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             26. .1687
FT                   /*tag=  a
XX
PN   WO2002103020-A1.
XX
PD   27-DEC-2002.
XX
PF   14-JUN-2002; 2002WO-JP005942.
XX
PR   15-JUN-2001; 2001JP-00182654.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Koyama N,  Tanida S,  Yamamoto K;
XX
DR   WPI; 2003-157045/15.
DR   P-PSDB; ABP60079.
XX
PT   Novel disease-associated gene of the RGS gene family and its product,
PT   applicable in diagnosis of and screening for drugs for heart diseases,
PT   cancers and omentopathy.
XX
PS   Example 3; Page 85-86; 96pp; Japanese.
XX
CC   The invention relates to a novel disease associated gene and its uses.
CC   The gene and its encoded protein are useful for diagnosis of and
CC   screening for drugs for heart diseases, cancers and omentopathy. The
CC   current sequence represents a human gene sequence relative to the
CC   invention
XX
SQ   Sequence 1761 BP; 441 A; 441 C; 504 G; 375 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 1655.8;  DB 7;  Length 1761;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         26 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 85

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 145

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        146 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 205

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 265

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        266 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 325

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 385

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 445

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        446 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 505

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        506 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 565

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        566 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 625

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        626 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 685

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        686 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 745

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        746 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 805

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        806 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 865

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        866 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 925

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        926 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 985

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        986 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1045

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1046 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1105

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1106 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1165

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1166 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1225

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1226 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1285

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1286 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1345

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1346 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1405
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Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1406 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1465

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1466 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1525

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1526 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1585

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1586 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1645

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1646 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1684

RESULT 6
ADC39221
ID   ADC39221 standard; cDNA; 1821 BP.
XX
AC   ADC39221;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Novel human NOVX polypeptide coding sequence SEQ ID NO: 165.
XX
KW   ds; gene; antidiabetic; cytostatic; immunomodulator; anorectic;
KW   antilipemic; nootropic; neuroprotective; immunostimulant;
KW   antiparkinsonian; anti-HIV; antiasthmatic; antiinflammatory; hypotensive;
KW   antiarteriosclerotic; hemostatic; osteopathic; gene therapy.; NOVX;
KW   diabetes; obesity; cancer; lymphoma; uterus cancer; prostate cancer;
KW   dyslipidemia; anorexia; wasting disorder; Alzheimer's disease;
KW   Parkinson's disorder; cachexia; cardiomyopathy; AIDS; asthma;
KW   Crohn's disease; multiple sclerosis; hypertension; atherosclerosis;
KW   hemophilia; graft-versus-host disease;
KW   Albright hereditary osteodystrophy.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             73. .1732
FT                   /*tag=  a
XX
PN   WO2003010327-A2.
XX
PD   06-FEB-2003.
XX
PF   02-MAY-2002; 2002WO-US014199.
XX
PR   02-MAY-2001; 2001US-0288063P.
PR   03-MAY-2001; 2001US-0288395P.
PR   07-MAY-2001; 2001US-0289087P.
PR   09-MAY-2001; 2001US-0289817P.
PR   09-MAY-2001; 2001US-0289818P.
PR   11-MAY-2001; 2001US-0290194P.
PR   14-MAY-2001; 2001US-0290753P.
PR   15-MAY-2001; 2001US-0291181P.
PR   16-MAY-2001; 2001US-0291243P.
PR   18-MAY-2001; 2001US-0292001P.
PR   21-MAY-2001; 2001US-0292374P.
PR   22-MAY-2001; 2001US-0292587P.
PR   23-MAY-2001; 2001US-0293107P.
PR   25-MAY-2001; 2001US-0293747P.
PR   29-MAY-2001; 2001US-0294109P.
PR   29-MAY-2001; 2001US-0294110P.
PR   30-MAY-2001; 2001US-0294434P.
PR   31-MAY-2001; 2001US-0294827P.
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PR   12-JUL-2001; 2001US-0304879P.
PR   31-JUL-2001; 2001US-0308901P.
PR   14-AUG-2001; 2001US-0312270P.
PR   17-AUG-2001; 2001US-0313416P.
PR   10-SEP-2001; 2001US-0318463P.
PR   27-SEP-2001; 2001US-0325683P.
PR   18-OCT-2001; 2001US-0330292P.
PR   28-NOV-2001; 2001US-0333873P.
PR   03-DEC-2001; 2001US-0336909P.
PR   03-DEC-2001; 2001US-0337552P.
PR   21-FEB-2002; 2002US-0359245P.
PR   01-MAY-2002; 2002US-00136826.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Miller CE,  Kekuda R,  Malyankar UM,  Li L,  Pena CEA,  Spytek KA;
PI   Gorman L,  Guo X,  Fernandes ER,  Smithson G,  Stone DJ,  Zerhusen BD;
PI   Patturajan M,  Anderson DW,  Mezes PS,  Peyman JA,  Macdougall JR;
PI   Padigaru M,  Rastelli L,  Shenoy SG,  Gerlach VL,  Shimkets RA,  Zhong M;
PI   Edinger SR,  Ellerman K;
XX
DR   WPI; 2003-239445/23.
DR   P-PSDB; ADC39222.
XX
PT   New NOVX polypeptides and polynucleotides, useful in gene therapy,
PT   particularly for treating or preventing a syndrome associated with a
PT   human disease e.g. diabetes, obesity, cancer, Alzheimer's disease,
PT   hypertension or hemophilia.
XX
PS   Claim 20; SEQ ID NO 165; 748pp; English.
XX
CC   The invention relates to new isolated NOVX polypeptides, the genes
CC   encoding them or sequences having at least 95% identity to the amino acid
CC   or nucleotide sequences. The NOVX polypeptide is useful as a therapeutic,
CC   particularly in the manufacture of a medicament for treating a syndrome
CC   associated with a human disease, which includes a pathology associated
CC   with NOVX polypeptide. The NOVX polypeptide is particularly useful for
CC   treating, preventing or alleviating pathology associated with NOVX
CC   polypeptide in a mammal, e.g. a human. The NOVX nucleic acid and
CC   polypeptide are especially useful for treating or preventing e.g.
CC   diabetes, obesity, cancers (e.g. lymphoma, uterus cancer or prostate
CC   cancer), dyslipidemias, anorexia, wasting disorders, Alzheimer's disease,
CC   Parkinson's disorder, cachexia, cardiomyopathy, AIDS, asthma, Crohn's
CC   disease, multiple sclerosis, hypertension, atherosclerosis, hemophilia,
CC   graft-versus-host disease or Albright hereditary osteodystrophy. The DNA
CC   encoding the protein is useful in gene therapy for treating the above
CC   conditions. These are also useful in developing powerful assay system for
CC   functional analysis of various human disorders, as well as in diagnostic
CC   applications. This sequence represents one of the NOVX genes of the
CC   invention.
XX
SQ   Sequence 1821 BP; 453 A; 459 C; 524 G; 385 T; 0 U; 0 Other;

  Query Match              99.8%;  Score 1655.8;  DB 9;  Length 1821;
  Best Local Similarity    99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 132

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 192

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 252

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 312
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Qy          241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          313 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 372

Qy          301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          373 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 432

Qy          361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          433 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 492

Qy          421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
                |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db          493 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 552

Qy          481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          553 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 612

Qy          541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          613 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 672

Qy          601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          673 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 732

Qy          661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          733 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 792

Qy          721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          793 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 852

Qy          781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          853 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 912

Qy          841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          913 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 972

Qy          901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          973 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1032

Qy          961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1033 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1092

Qy         1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1093 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1152

Qy         1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1153 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1212

Qy         1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1213 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1272

Qy         1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1273 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1332

Qy         1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1333 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1392

Qy         1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1393 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1452

Qy         1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1453 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1512

Qy         1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1513 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1572

Qy         1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1573 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1632

Qy         1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1633 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1692

Qy         1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
                |||||||||||||||||||||||||||||||||||||||
Db         1693 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1731


RESULT 7
AAH78799
ID   AAH78799 standard; cDNA; 2249 BP.
XX
AC   AAH78799;
XX
DT   08-MAR-2002  (first entry)
XX
DE   Human G-protein coupled receptor kinase 3 cDNA sequence.
XX
KW   G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
KW   drug screening; gene expression characterisation; NHP;
KW   novel human protein.
XX
OS   Homo sapiens.
XX
PN   WO200168869-A2.
XX
PD   20-SEP-2001.
XX
PF   08-MAR-2001; 2001WO-US007500.
XX
PR   10-MAR-2000; 2000US-0188449P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Walke DW,  Wilganowski NL,  Turner CA;
XX
DR   WPI; 2001-570872/64.
XX
PT   New polynucleotides encoding human proteins that share sequence
PT   similarity with animal kinases e.g. G-protein coupled receptor kinases,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Disclosure; Page 33-34; 34pp; English.
XX
CC   The present cDNA sequence encodes a human G-protein coupled receptor
CC   kinase (GRK), also designated NHP (novel human protein) in the
CC   specification, which is shown in the sequence listing. The invention
CC   comprises novel human nucleotide and protein sequences which have
CC   similarity to G-protein coupled receptor kinases. Oligonucleotides
CC   derived from the nucleotides of the invention are useful as hybridisation
CC   probes for screening libraries and assessing gene expression patterns.
CC   The nucleotides of the invention are also useful in drug screening and
CC   gene therapy for the modulation of GRK expression. The nucleotides of the
CC   invention can be used to genetically engineer host cells to express GRK
CC   products in vivo. The nucleotide sequences of the invention are also
CC   useful in addressable arrays for identifying and characterising the
CC   temporal and tissue specific expression of a gene and in microarrays to
CC   screen collections of genetic material from patients who have a
CC   particular medical condition. The proteins of the invention are useful
CC   for generating antibodies, as reagents in diagnostic assays, for
CC   identifying other cellular gene products related to GRK, and as reagents
CC   in assays for screening for compounds that are useful in the treatment of
CC   mental, biological or medical disorders/diseases
XX
SQ   Sequence 2249 BP; 582 A; 577 C; 608 G; 482 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 1655.8;  DB 4;  Length 2249;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 413

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 473

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 533

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 593

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        594 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 653

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        654 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 713

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        714 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 773

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        774 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 833

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 893

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 953

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 1013

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1014 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1073

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1074 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1133

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1134 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1193

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1194 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1253

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1254 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1313

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1373

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1374 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1433

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1434 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1493

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1494 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1553

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1554 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1613

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1614 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1673

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1674 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1733

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1734 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1793

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1794 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1853

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1854 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1913

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1914 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1974 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 2012


RESULT 8
ACC44827
ID   ACC44827 standard; cDNA; 3186 BP.
XX
AC   ACC44827;
XX
DT   04-JUN-2003  (first entry)
XX
DE   Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:4.
XX
KW   Human; G protein coupled receptor kinase; GRK; cytostatic; antidiabetic;
KW   neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiant;
KW   vasotropic; antiasthmatic; gene therapy; cancer; diabetes; CNS disorder;
KW   central nervous system disorder; cardiovascular disorder; asthma; COPD;
KW   chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;
KW   Alzheimer's disease; Parkinson's disease; congestive heart failure;
KW   myocardial infarction; ischaemic disease; hypertensive vascular disease;
KW   gene; ss.
XX
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OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             85. .1746
FT                   /*tag=  a
FT                   /product= "G protein-coupled receptor kinase (GRK)"
XX
PN   WO2003018815-A2.
XX
PD   06-MAR-2003.
XX
PF   19-AUG-2002; 2002WO-EP009235.
XX
PR   21-AUG-2001; 2001US-0313464P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; 2003-278669/27.
DR   P-PSDB; ABP96709.
XX
PT   New G-protein coupled receptor kinase polypeptides and polynucleotides,
PT   useful in identifying modulators of the enzyme for treating cancer,
PT   diabetes, a central nervous system disorder, a cardiovascular disorder or
PT   asthma.
XX
PS   Claim 1; Fig 11; 129pp; English.
XX
CC   The present sequence encodes a human G protein-coupled receptor kinase
CC   (GRK) protein (I). (I) has cytostatic, antidiabetic, neuroprotective,
CC   nootropic, cardiovascular, anti-Parkinsonian, cardiant, vasotropic and
CC   antiasthmatic activities, and can be used in gene therapy. (I) can be
CC   regulated to treat cancer, diabetes, a central nervous system (CNS)
CC   disorder (e.g. anxiety or mood disorders, Alzheimer's disease and
CC   Parkinson's disease), cardiovascular disorders (e.g. congestive heart
CC   failure, myocardial infarction, ischaemic diseases of the heart or
CC   hypertensive vascular disease), asthma and chronic obstructive pulmonary
CC   disorder (COPD). GRK molecules are useful in screening for agents that
CC   regulate or decease the activity of a GRK. GRK sequences may also be used
CC   for detecting diseases and abnormalities or susceptibility to diseases
CC   and abnormalities related to the presence of mutations in the nucleic
CC   acid sequences that encode the GRK enzyme
XX
SQ   Sequence 3186 BP; 857 A; 737 C; 784 G; 808 T; 0 U; 0 Other;

  Query Match             99.8%;  Score 1655.8;  DB 7;  Length 3186;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1657;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 144

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 204

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        205 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 264

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        265 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 324

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        325 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 384

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        385 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 444

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 504

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        505 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 564

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        565 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 624

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        625 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 684

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        685 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 744

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        745 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 804

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        805 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 864

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        865 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 924

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        925 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 984

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        985 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1044

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1045 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1104

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1105 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1164

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1165 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1224

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1225 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1284

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1285 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1344

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1345 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1404

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1405 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1464

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1465 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1524
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Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1525 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGTGGAATTTGATGACAAA 1584

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1585 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1644

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1645 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1704

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1705 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1743


RESULT 9
AAH78797
ID   AAH78797 standard; cDNA; 1662 BP.
XX
AC   AAH78797;
XX
DT   08-MAR-2002  (first entry)
XX
DE   Human G-protein coupled receptor kinase 1 cDNA sequence.
XX
KW   G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
KW   drug screening; gene expression characterisation; NHP;
KW   novel human protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "G-protein coupled receptor kinase 1"
XX
PN   WO200168869-A2.
XX
PD   20-SEP-2001.
XX
PF   08-MAR-2001; 2001WO-US007500.
XX
PR   10-MAR-2000; 2000US-0188449P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Walke DW,  Wilganowski NL,  Turner CA;
XX
DR   WPI; 2001-570872/64.
DR   P-PSDB; AAG77815.
XX
PT   New polynucleotides encoding human proteins that share sequence
PT   similarity with animal kinases e.g. G-protein coupled receptor kinases,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Claim 1; Page 30; 34pp; English.
XX
CC   The present cDNA sequence encodes a human G-protein coupled receptor
CC   kinase (GRK), also designated NHP (novel human protein) in the
CC   specification, which is claimed in the invention. The invention comprises
CC   novel human nucleotide and protein sequences which have similarity to G-
CC   protein coupled receptor kinases. Oligonucleotides derived from the
CC   nucleotides of the invention are useful as hybridisation probes for
CC   screening libraries and assessing gene expression patterns. The
CC   nucleotides of the invention are also useful in drug screening and gene
CC   therapy for the modulation of GRK expression. The nucleotides of the
CC   invention can be used to genetically engineer host cells to express GRK
CC   products in vivo. The nucleotide sequences of the invention are also
CC   useful in addressable arrays for identifying and characterising the
CC   temporal and tissue specific expression of a gene and in microarrays to
CC   screen collections of genetic material from patients who have a
CC   particular medical condition. The proteins of the invention are useful
CC   for generating antibodies, as reagents in diagnostic assays, for
CC   identifying other cellular gene products related to GRK, and as reagents
CC   in assays for screening for compounds that are useful in the treatment of
CC   mental, biological or medical disorders/diseases
XX
SQ   Sequence 1662 BP; 420 A; 410 C; 479 G; 352 T; 0 U; 1 Other;

  Query Match             99.8%;  Score 1655.4;  DB 4;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1656;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
```

```
Qy       901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy       961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy      1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy      1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy      1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy      1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy      1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy      1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy      1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy      1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy      1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy      1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy      1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
             |||||||||||||||||||||||||||||||||||||||
Db      1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
```

```
RESULT 10
AAD28071
ID   AAD28071 standard; cDNA; 1662 BP.
XX
AC   AAD28071;
XX
DT   22-APR-2002  (first entry)
XX
DE   Human kinase cDNA.
XX
KW   Human; kinase; G-protein coupled receptor kinase; tissue differentiation;
KW   chromosome 3; therapeutic; immune response; drug screening; enzyme; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "Human kinase protein"
XX
PN   WO200192496-A2.
XX
PD   06-DEC-2001.
XX
PF   31-MAY-2001; 2001WO-US017510.
XX
PR   01-JUN-2000; 2000US-0208331P.
PR   18-DEC-2000; 2000US-00738894.
XX
PA   (APPL-) APPLERA CORP.
XX
PI   Guegler K,  Di Francesco V,  Beasley EM;
XX
DR   WPI; 2002-130533/17.
DR   P-PSDB; AAE17136.
XX
PT   New isolated human kinase proteins and nucleic acids, useful as a major
PT   target for drug action and development, particularly for screening
PT   modulators of the kinase peptides.
XX
PS   Claim 4; Fig 1; 87pp; English.
XX
CC   The invention relates to human kinase proteins that are related to G-
CC   protein coupled receptor kinase subfamily. Human kinase gene is located
CC   on chromosome 3. The kinase peptide and nucleic acid are useful in the
CC   development of human therapeutic and diagnostic compositions. The peptide
CC   is useful as a major target for drug action and development, and is
CC   valuable to the field of pharmaceutical development to identify and
CC   characterise modulators of the kinase. The proteins may also be used to
CC   raise antibodies or to elicit an immune response, as a reagent in assays
CC   designed to quantitatively determine levels of the protein in biological
CC   fluids and as markers for tissues in which the corresponding protein is
CC   preferentially expressed (either constitutively or at a particular stage
CC   of tissue differentiation or development or in a disease state). The
CC   kinase proteins are also useful for providing a target for diagnosing a
CC   disease or predisposition to disease mediated by the peptide. The nucleic
CC   acid molecules are useful for probes, primers, chemical intermediates and
CC   in biological assays. The nucleic acids are also useful in making vectors
CC   containing the gene regulatory regions of the nucleic acid molecules and
CC   for drug screening to identify compounds that modulate kinase nucleic
CC   acid expression. The present sequence is human kinase cDNA expressed in
CC   skins, germinal center B cells, colon, kidney and lung
XX
SQ   Sequence 1662 BP; 419 A; 411 C; 480 G; 352 T; 0 U; 0 Other;

  Query Match             99.7%;  Score 1654.2;  DB 6;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1656;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy        61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy       121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy       181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy       241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy       301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
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Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659


RESULT 11
AAS06702
ID   AAS06702 standard; cDNA; 1662 BP.
XX
AC   AAS06702;
XX
DT   12-SEP-2001  (first entry)
XX
DE   Polynucleotide sequence encoding human protein kinase #2.
XX
KW   Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
KW   metabolic disorder; immune related disease; neurological disorder;
KW   neurodegenerative disorder; inflammatory disorder; infectious disease;
KW   reproductive disorder; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   WO200138503-A2.
XX
PD   31-MAY-2001.
XX
PF   22-NOV-2000; 2000WO-US032085.
XX
PR   24-NOV-1999;   99US-0167482P.
XX
PA   (SUGE-) SUGEN INC.
XX
PI   Plowman GD,  Whyte D,  Manning G,  Sudarsanam S,  Martinez R;
PI   Flanagan P,  Clary D;
XX
DR   WPI; 2001-343950/36.
DR   P-PSDB; AAU03502.
XX
PT   Nucleic acids encoding human kinase polypeptides, useful for preventing
PT   diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT   neuronal-associated diseases, and microbial infections.
XX
PS   Example 1; Fig 1; 433pp; English.
XX
CC   AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
CC   protein kinases have been identified as members of the tyrosine or
CC   serine/threonine kinase (PTK and STK) families. The polynucleotides
CC   encoding protein kinases and the polypeptides may be used in the
CC   prevention, diagnosis and treatment of diseases associated with
CC   inappropriate kinase expression. For example, they may be used to treat
CC   cancers (especially cancers of haematopoietic origin), cardiovascular
CC   disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC   immune related diseases (e.g. rheumatoid arthritis), neurological
CC   disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC   Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC   disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC   Additionally, polynucleotides encoding protein kinases may be used for
CC   gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC   polypeptides may be used as antigens in the production of antibodies
CC   against the protein kinases and in assays to identify modulators of
CC   protein kinase expression and activity
XX
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SQ   Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;

  Query Match             99.6%;  Score 1652.6;  DB 4;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1655;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGGGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
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Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
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Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
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Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
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Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAAGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659


RESULT 12
ACC44826
ID   ACC44826 standard; cDNA; 1662 BP.
XX
AC   ACC44826;
XX
DT   04-JUN-2003  (first entry)
XX
DE   Human G protein-coupled receptor kinase encoding cDNA SEQ ID NO:1.
XX
KW   Human; G protein coupled receptor kinase; GRK; cytostatic; antidiabetic;
KW   neuroprotective; nootropic; cardiovascular; anti-Parkinsonian; cardiant;
KW   vasotropic; antiasthmatic; gene therapy; cancer; diabetes; CNS disorder;
KW   central nervous system disorder; cardiovascular disorder; asthma; COPD;
KW   chronic obstructive pulmonary disorder; anxiety; mood disorder; enzyme;
KW   Alzheimer's disease; Parkinson's disease; congestive heart failure;
KW   myocardial infarction; ischaemic disease; hypertensive vascular disease;
KW   gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1662
FT                   /*tag=  a
FT                   /product= "G protein-coupled receptor kinase (GRK)"
XX
PN   WO2003018815-A2.
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XX
PD   06-MAR-2003.
XX
PF   19-AUG-2002; 2002WO-EP009235.
XX
PR   21-AUG-2001; 2001US-0313464P.
XX
PA   (FARB ) BAYER AG.
XX
PI   Xiao Y;
XX
DR   WPI; 2003-278669/27.
DR   P-PSDB; ABP96707.
XX
PT   New G-protein coupled receptor kinase polypeptides and polynucleotides,
PT   useful in identifying modulators of the enzyme for treating cancer,
PT   diabetes, a central nervous system disorder, a cardiovascular disorder or
PT   asthma.
XX
PS   Claim 1; Fig 1; 129pp; English.
XX
CC   The present sequence encodes a human G protein-coupled receptor kinase
CC   (GRK) protein (I). (I) has cytostatic, antidiabetic, neuroprotective,
CC   nootropic, cardiovascular, anti-Parkinsonian, cardiant, vasotropic and
CC   antiasthmatic activities, and can be used in gene therapy. (I) can be
CC   regulated to treat cancer, diabetes, a central nervous system (CNS)
CC   disorder (e.g. anxiety or mood disorders, Alzheimer's disease and
CC   Parkinson's disease), cardiovascular disorders (e.g. congestive heart
CC   failure, myocardial infarction, ischaemic diseases of the heart or
CC   hypertensive vascular disease), asthma and chronic obstructive pulmonary
CC   disorder (COPD). GRK molecules are useful in screening for agents that
CC   regulate or decease the activity of a GRK. GRK sequences may also be used
CC   for detecting diseases and abnormalities or susceptibility to diseases
CC   and abnormalities related to the presence of mutations in the nucleic
CC   acid sequences that encode the GRK enzyme
XX
SQ   Sequence 1662 BP; 421 A; 411 C; 479 G; 351 T; 0 U; 0 Other;

  Query Match             99.6%;  Score 1652.6;  DB 7;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1655;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGGGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAAGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
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Qy        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
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Db        1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
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Db        1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659


RESULT 13
ABZ56934
ID   ABZ56934 standard; DNA; 1191 BP.
XX
AC   ABZ56934;
XX
DT   04-APR-2003  (first entry)
XX
DE   Human RGSNo9 encoding DNA # SEQ ID 2.
XX
KW   Human; RGSNo9; heart disease; cancer; omentopathy; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1191
FT                   /*tag=  a
FT                   /product= "RGSNo9"
XX
PN   WO2002103020-A1.
XX
PD   27-DEC-2002.
XX
PF   14-JUN-2002; 2002WO-JP005942.
XX
PR   15-JUN-2001; 2001JP-00182654.
XX
PA   (TAKE ) TAKEDA CHEM IND LTD.
XX
PI   Koyama N,  Tanida S,  Yamamoto K;
XX
DR   WPI; 2003-157045/15.
DR   P-PSDB; ABP60078.
XX
PT   Novel disease-associated gene of the RGS gene family and its product,
PT   applicable in diagnosis of and screening for drugs for heart diseases,
PT   cancers and omentopathy.
XX
PS   Claim 6; Page 81-82; 96pp; Japanese.
XX
CC   The invention relates to a novel disease associated gene and its uses.
CC   The gene and its encoded protein are useful for diagnosis of and
CC   screening for drugs for heart diseases, cancers and omentopathy. The
CC   current sequence represents the human RGSNo9 encoding DNA sequence
XX
SQ   Sequence 1191 BP; 274 A; 320 C; 363 G; 234 T; 0 U; 0 Other;

  Query Match             71.6%;  Score 1187.8;  DB 7;  Length 1191;
  Best Local Similarity   99.8%;  Pred. No. 3.7e-286;
  Matches 1189;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
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Db           1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
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Db         121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy         181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy         241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy         361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy         421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
               |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db         421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
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Db         541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
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Db         601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
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Db         661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
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Db         841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
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Db        1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy        1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
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Db        1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAG 1191
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Db        1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAG 1191


RESULT 14
AAD46351
ID   AAD46351 standard; cDNA; 1486 BP.
XX
AC   AAD46351;
```

```
XX
DT   27-JAN-2003  (first entry)
XX
DE   Human cone opsin kinase (GRK7) OK6 splice variant cDNA.
XX
KW   Human; enzyme; cone opsin kinase; G-protein coupled receptor kinase 7;
KW   GRK7; cone visual signalling; visual sensitivity; visual resolution;
KW   night blindness; colour blindness; Oguchi disease; Pineal gland activity;
KW   chronobiological desynchrony; depression; anxiety; memory loss; headache;
KW   mental fogginess; fatigue; jet lag; circadian rhythm; ophthalmological;
KW   gene therapy; antidepressant; analgesic; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1062
FT                   /*tag=  a
FT                   /product= "Human GRK7 OK6 splice variant protein"
XX
PN   WO200272541-A2.
XX
PD   19-SEP-2002.
XX
PF   07-MAR-2002; 2002WO-US007025.
XX
PR   07-MAR-2001; 2001US-0274006P.
XX
PA   (IMMV ) IMMUNEX CORP.
XX
PI   Bird TA,  Spencer M,  Mosley BA;
XX
DR   WPI; 2002-723307/78.
DR   P-PSDB; AAE28953.
XX
PT   Identifying compounds that alter inhibition of cone opsin kinase
PT   polypeptide activity for treating a conditions related to cone visual
PT   signaling, comprises mixing a compound with a cone opsin kinase and with
PT   an inhibitory polypeptide.
XX
PS   Example 4; Page 48-49; 61pp; English.
XX
CC   The present invention relates to novel human cone opsin kinase (G-protein
CC   coupled receptor kinase 7; GRK7) and their corresponding polynucleotides.
CC   The invention further relates to a method of identifying compounds that
CC   alter the inhibition of GRK7 polypeptide activity which involves mixing a
CC   test compound with GRK7 protein and an inhibitory polypeptide and
CC   determining if the test compound alters the inhibition of GRK7 protein
CC   activity by the inhibitory polypeptide. GRk7 sequences are useful for
CC   treating conditions related to cone visual signalling (e.g., night
CC   blindness, colour blindness, difficulty with colour vision, visual
CC   sensitivity, visual resolution or in adapting to changes in light
CC   intensity, Oguchi disease or dominant congenital stationary night
CC   blindness), Pineal gland activity (e.g., chronobiological desynchrony,
CC   depression, anxiety, mental fogginess, memory loss, headaches, fatigue,
CC   or jet lag). Agonists of GRK7 polypeptide activity may be used to treat
CC   or ameliorate symptoms of a disease for which increased GRK7 polypeptide
CC   activity is beneficial, e.g., decreased colour sensitivity or other cone
CC   photoreceptor-mediated diseases. The GRK7 proteins are also useful in the
CC   preparation of a medicament for treating a condition or disease related
CC   to cone photoreceptor visual signaling or circadian rhythm, as molecular
CC   probes to screen for inherited defects in colour vision, circadian rhythm
CC   and vision resolution. They are also used as gene therapy tools for
CC   individuals with such disorders. The present sequence is human GRK7 OK6
CC   splice variant cDNA
XX
SQ   Sequence 1486 BP; 353 A; 387 C; 434 G; 312 T; 0 U; 0 Other;

  Query Match             66.0%;  Score 1094.2;  DB 6;  Length 1486;
  Best Local Similarity   83.2%;  Pred. No. 9.5e-263;
  Matches 1381;  Conservative    0;  Mismatches    3;  Indels  275;  Gaps    1;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
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Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
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Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
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Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
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Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
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Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
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Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
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Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              |||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAG------------------------------- 1049

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Db       1050 ------------------------------------------------------------ 1049
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Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Db       1050 ------------------------------------------------------------ 1049

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Db       1050 ------------------------------------------------------------ 1049

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Db       1050 ------------------------------------------------------------ 1049

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1050 ----GAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1105

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
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Db       1106 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1165

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1166 AAAGACATCGCCGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1225

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
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Db       1226 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1285

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1286 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1345

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1346 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1384
```

RESULT 15

```
AAH78798
ID   AAH78798 standard; cDNA; 1062 BP.
XX
AC   AAH78798;
XX
DT   08-MAR-2002  (first entry)
XX
DE   Human G-protein coupled receptor kinase 2 cDNA sequence.
XX
KW   G-protein coupled receptor kinase; GRK; human; ss; gene therapy;
KW   drug screening; gene expression characterisation; NHP;
KW   novel human protein.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1062
FT                   /*tag=  a
FT                   /product= "G-protein coupled receptor kinase 2"
XX
PN   WO200168869-A2.
XX
PD   20-SEP-2001.
XX
PF   08-MAR-2001; 2001WO-US007500.
XX
PR   10-MAR-2000; 2000US-0188449P.
XX
PA   (LEXI-) LEXICON GENETICS INC.
XX
PI   Walke DW,  Wilganowski NL,  Turner CA;
XX
DR   WPI; 2001-570872/64.
DR   P-PSDB; AAG77816.
XX
PT   New polynucleotides encoding human proteins that share sequence
PT   similarity with animal kinases e.g. G-protein coupled receptor kinases,
PT   useful for drug screening, diagnosis and in gene therapy of biological
PT   disorders.
XX
PS   Claim 4; Page 32; 34pp; English.
XX
CC   The present cDNA sequence encodes a human G-protein coupled receptor
CC   kinase (GRK), also designated NHP (novel human protein) in the
CC   specification, which is claimed in the invention. The invention comprises
CC   novel human nucleotide and protein sequences which have similarity to G-
CC   protein coupled receptor kinases. Oligonucleotides derived from the
CC   nucleotides of the invention are useful as hybridisation probes for
CC   screening libraries and assessing gene expression patterns. The
CC   nucleotides of the invention are also useful in drug screening and gene
CC   therapy for the modulation of GRK expression. The nucleotides of the
CC   invention can be used to genetically engineer host cells to express GRK
CC   products in vivo. The nucleotide sequences of the invention are also
CC   useful in addressable arrays for identifying and characterising the
CC   temporal and tissue specific expression of a gene and in microarrays to
CC   screen collections of genetic material from patients who have a
CC   particular medical condition. The proteins of the invention are useful
CC   for generating antibodies, as reagents in diagnostic assays, for
CC   identifying other cellular gene products related to GRK, and as reagents
CC   in assays for screening for compounds that are useful in the treatment of
CC   mental, biological or medical disorders/diseases
XX
SQ   Sequence 1062 BP; 237 A; 296 C; 330 G; 199 T; 0 U; 0 Other;

  Query Match             63.1%;  Score 1046.8;  DB 4;  Length 1062;
  Best Local Similarity   99.8%;  Pred. No. 5.6e-251;
  Matches 1048;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
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Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
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Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
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Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
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Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
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Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
```

```
Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
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Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
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Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
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Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1050
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Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1050

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Job time : 450.751 secs
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                     GenCore version 5.1.6
              Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:         August 13, 2004, 12:57:35 ; Search time 2906.37 Seconds
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Title:          US-10-044-205A-3
Perfect score:  1659
Sequence:       1 atggtggacatgggggccct..........ctggcgtgtgtttgttattg 1659

Scoring table:  IDENTITY_NUC
                Gapop 10.0 , Gapext 1.0

Searched:       27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters:       55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                  SUMMARIES
                        %
Result               Query
  No.     Score      Match Length DB  ID                Description
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     1    398.6      24.0   2978  11  AK051405          AK051405 Mus muscu
     2      375      22.6   2989  11  BC057206          BC057206 Mus muscu
c    3    311.8      18.8   1201  13  BX404586          BX404586 BX404586
     4    311.6      18.8   2329  11  BC027597          BC027597 Homo sapi
c    5      307      18.5    917  13  BX392018          BX392018 BX392018
     6    304.6      18.4   1721  29  AY406080          AY406080 Homo sapi
     7    300.2      18.1   1058  13  BQ057469          BQ057469 AGENCOURT
     8    299.2      18.0   1019  13  BQ061148          BQ061148 AGENCOURT
     9      295      17.8   1721  29  AY406082          AY406082 Mus muscu
    10    281.8      17.0    934  13  BU526699          BU526699 AGENCOURT
    11    280.6      16.9    903  13  BU146436          BU146436 AGENCOURT
    12    272.2      16.4    560  12  BM794145          BM794145 K-EST0075
    13    272.2      16.4    601  12  BM697499          BM697499 UI-E-DX0-
    14    272.2      16.4   1017  13  BQ061150          BQ061150 AGENCOURT
c   15    270.6      16.3    815   9  AI934968          AI934968 wd17a07.x
    16    269.6      16.3    990  13  BQ071614          BQ071614 AGENCOURT
    17    269.2      16.2    857  13  BU527897          BU527897 AGENCOURT
    18    268.8      16.2    968  13  BQ066445          BQ066445 AGENCOURT
    19      267      16.1   1028  13  BQ063841          BQ063841 AGENCOURT
c   20    265.6      16.0    696  10  BE677821          BE677821 7f63e10.x
    21    265.4      16.0    998  13  BQ057613          BQ057613 AGENCOURT
    22    264.8      16.0   1032  12  BM472080          BM472080 AGENCOURT
    23    264.4      15.9   1034  10  BF568334          BF568334 602184519
    24    264.2      15.9    851  13  BQ230423          BQ230423 AGENCOURT
    25    264.2      15.9   1622  29  AY406081          AY406081 Pan trogl
    26    263.6      15.9    826  12  BG828886          BG828886 602752869
    27      263      15.9    777  10  BE795217          BE795217 601592482
c   28      258      15.6    713  10  AW173009          AW173009 xj82a11.x
    29      258      15.6   1057  13  BQ071329          BQ071329 AGENCOURT
    30      256      15.4    543  10  BE394617          BE394617 601311853
    31    254.8      15.4    707  12  BG823182          BG823182 602726540
c   32    253.6      15.3    769  13  BW013848          BW013848 BW013848
    33    252.8      15.2    892  14  CB195631          CB195631 AGENCOURT
    34    252.4      15.2    838  13  BX849055          BX849055 BX849055
c   35    250.2      15.1    810  13  BW085647          BW085647 BW085647
c   36      249      15.0    676   9  AI640213          AI640213 wa30e01.x
c   37    247.8      14.9    792  13  BX684426          BX684426 BX684426
    38    244.4      14.7    660  13  BQ520195          BQ520195 NISC_nl03
    39    243.2      14.7   1351  13  BQ213536          BQ213536 AGENCOURT
    40    240.2      14.5    995  13  BQ056240          BQ056240 AGENCOURT
    41    239.4      14.4    569  12  BM712420          BM712420 UI-E-DW1-
c   42    239.4      14.4    658   9  AI738477          AI738477 wi32d04.x
c   43    239.2      14.4    724  13  BW014695          BW014695 BW014695
    44    238.6      14.4    942  10  BE727456          BE727456 601560667
c   45      238      14.3    742  10  BF439363          BF439363 nab63e06.


                                  ALIGNMENTS


RESULT 1
AK051405
LOCUS       AK051405                2978 bp    mRNA    linear   HTC 20-SEP-2003
DEFINITION  Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
            enriched library, clone:D130046K22 product:G PROTEIN-COUPLED
            RECEPTOR KINASE GRK6 (EC 2.7.1.-) homolog [Mus musculus], full
            insert sequence.
ACCESSION   AK051405
VERSION     AK051405.1  GI:26094516
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
  PUBMED    11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 2978)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
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                     /db_xref="MGI:2419686"
                     /db_xref="taxon:10090"
                     /clone="D130046K22"
                     /tissue_type="spinal ganglion"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="12 days embryo"
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                     /note="G PROTEIN-COUPLED RECEPTOR KINASE GRK6 (EC 2.7.1.-)
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                     putative"
ORIGIN
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  Best Local Similarity   55.5%;  Pred. No. 7.7e-80;
  Matches  832;  Conservative    0;  Mismatches  659;  Indels    8;  Gaps    3;

Qy          98 GGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGT 157
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Db         248 GGCGCCAGATGCTGCAGTTCCCCCATATCAGCCAGTGTGAGGAGCTTCGACTCAGCCTTG 307

Qy         158 CCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACT 217
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Db         308 AGCGTGACTACCACAGCCTATGTGAGCGCCAGCCCATTGGGCGCCTGTTATTTCGTGAGT 367

Qy         218 TCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACT 277
               ||   || ||    ||   | |   |  |    |  ||||||| || |  |||    | |
Db         368 TCTGTGCTACGAGACCTGAGCTGACCCGGTGTACTGCCTTCCTGGATGGGGTGTCTGAAT 427

Qy         278 GGGAGCTGGCCGAGGAGGGACCCACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTT 337
                 ||| || ||   || |        ||||   | | ||  |   | ||  ||   |  |
Db         428 ATGAGGTGACCCCTGATGAGAAGCGGAAAGCATGTGGGCGCC---GACTAATGCAGAACT 484

Qy         338 GTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCA 397
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Db         485 TTCTGAGCCACACGGGTCCTGACCTCATCCCTGAAGTTCCACGGCAGCTGGTGAGTAACT 544

Qy         398 AGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTG 457
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Db         545 GTGCCCAGCGGCTAGAGGCAGGGACCCTGCAAAGACCTCTTCCAGGAGCTGACCCGGCTG 604

Qy         458 AGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACG 517
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Db         605 A--CCCACGAGTACCTGAGCACGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCA 662

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               ||   |||||||||||||||     | || | |||||||||| |  | ||    |||||
Db         663 ACCGTTTTCTGCAGTGGAAGTGGCTGGAAAGGCAACCAGTGACCAAAAACACCTTCAGGC 722

Qy         578 AGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACA 637
               ||| | |||| ||||| |||||||| ||||||||||||||||||  |||||||      |
Db         723 AGTACCGAGTCCTGGGCAAAGGTGGCTTTGGGGAGGTATGTGCCTGCCAGGTGCGGGCAA 782

Qy         638 CTGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCG 697
               | || |||||||| || || ||||||||||| |||||||||| | ||||||  |   || |
Db         783 CAGGCAAGATGTACGCATGCAAGAAACTGGAAAAGAAGCGGATAAAGAAGCGAAAGGGGG 842

Qy         698 AGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCT 757
               ||   |||||||||   || ||  | ||||||||||| || | |||    ||  | ||
Db         843 AGGCCATGGCTCTCAACGAGAAACAGATCTTGGAGAAAGTGAACAGTAGGTTTGTAGTGA 902

Qy         758 CTCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATG 817
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Qy         818 GGGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGG 877
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Db         963 GAGGTGACCTAAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTTCCTGAAGCACGTG 1022

Qy         878 TGATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCG 937
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Db        1023 CTGTCTTCTATGCTGCTGAGATCTGCTGTGGCCTGGAAGACCTGCACCGGGAACGCATTG 1082

Qy         938 TCTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTAT 997
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Db        1083 TGTACAGGGATCTAAAGCCAGAGAATATCCTTCTGGATGACCATGGCCACATTCGGATCT 1142

Qy         998 CTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAA 1057
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Db        1143 CGGACCTGGGACTGGCCGTGCATGTGCCTGAGGGCCAGACCATCAAAGGCCGTGTGGGCA 1202

Qy        1058 CCAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGG 1117
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Db        1203 CTGTGGGCTACATGGCTCCAGAGGTGGTGAGG---AATGAGCGCTACACGTTCAGTCCTG 1259

Qy        1118 ACTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAG 1177
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Qy       1178 ATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCA 1237
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Qy       1238 AATTCCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTA 1297
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Db       1380 AGTACACAGACCGCTTTTCCTCACAGGCGCGCTCACTCTGTTCTCAGCTTCTTAGCAAGG 1439

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Db       1440 ACCCTGCTGAGCGCCTGGGGTGTCGTGGAGGTGGCGCCCGTGAGGTAAAGGAGCACCCCC 1499

Qy       1358 TCTTTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGC 1417
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Qy       1418 CAGACCCTTCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTC 1477
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Db       1560 CTGATCCCCAGGCTATTTATTGCAAGGATGTCCTGGACATTGAACAGTTCTCTACAGTTA 1619

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Db       1620 AAGGTGTGGATCTGGAGCCCACAGACCAAGACTTCTACCAGAAGTTTGCCACAGGCAGTG 1679

Qy       1538 TTCCTATAGCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATGAC 1596
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Db       1680 TGTCCATCCCCTGGCAGAATGAGATGGTGGAGACCGAGTGCTTCCAGGAACTCAATGTC 1738

RESULT 2
BC057206
LOCUS       BC057206                2989 bp    mRNA    linear   HTC 19-NOV-2003
DEFINITION  Mus musculus G protein-coupled receptor kinase 6, mRNA (cDNA clone
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ACCESSION   BC057206
VERSION     BC057206.1  GI:34784381
KEYWORDS    HTC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2989)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
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            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
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            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
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            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  MEDLINE   22388257
   PUBMED   12477932
REFERENCE   2  (bases 1 to 2989)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-AUG-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
            Ph.D.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 123 Row: m Column: 10
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 7242151
            This clone has the following problem: frame shifted.
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ORIGIN

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Qy         15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74
              ||  || || ||| |  | || ||||| |     ||  |||||||| |       | | |
Db        170 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGTGGCGG 229

Qy         75 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
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Qy        132 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 191
               || | ||||||| || |  |  ||    |   ||| |||||||||| |||||||  |||||
Db        290 GTGTGAGGAGCTTCGACTCAGCCTTGAGCGTGACTACCACAGCCTATGTGAGCGCCAGCC 349

Qy        192 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 251
              ||| || ||||   | || ||||| |||   || ||    ||   | |   |  |    |
Db        350 CATTGGGCGCCTGTTATTTCGTGAGTTCTGTGCTACGAGACCTGAGCTGACCCGGTGTAC 409

Qy        252 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 311
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Db        410 TGCCTTCCTGGATGGGGTGTCTGAATATGAGGTGACCCCTGATGAGAAGCGGAAAGCATG 469

Qy        312 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 371
               | ||  |   | ||  ||   |  | |  |||   | | |  || |    |   |
Db        470 TGGGCGCC---GACTAATGCAGAACTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 526

Qy        372 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                | |   | |||   |||   | |  ||||| ||| || |   | | |     || |
Db        527 AGTTCCACGGCAGCTGGTGAGTAAC-TGTGCCCAGCGGCTAGAGCAGGGACCCTGCAAAG 585

Qy        432 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 491
                ||              |  ||||||  ||   |  | | ||     |   || |||
Db        586 ACCTCTTCCAGGAGCTGACCCGGCTGA--CCCACGAGTACCTGAGCACGGCCCCTTTTGC 643

Qy        492 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
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Db        644 CGACTACCTCGACAGCATCTACTTCAACCGTTTTCTGCAGTGGAAGTGGCTGGAAAGGCA 703

Qy        552 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
              ||||||| |  | ||   |||||   ||| | |||| ||||| |||||||| ||||||||
Db        704 ACCAGTGACCAAAAACACCTTCAGGCAGTACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 763

Qy        612 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
              |||  | ||                || || |||||||| || || ||||||||||| ||
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Qy        672 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 731
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Db        809 GAAGCGGATAAAGAAGCGAAAGGGGGAGGCCATGGCTCTCAACGAGAAACAGATCTTGGA 868

Qy        732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 791
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Db        869 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTAGCCTACGCCTATGAGACCAAGGATGCACT 928

Qy        792 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 851
               ||||| ||  |||   |||||||||| || ||||| ||||||||||||||| || ||||
Db        929 GTGCCTGGTGCTGACATTGATGAATGGAGGTGACCTAAAGTTCCACATCTACCACATGGG 988

Qy        852 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 911
              |  |  |||| |          || |   |||| ||  | ||  ||||   ||||||  |
Db        989 CCAGGCTGGCTTTCCTGAAGCACGTGCTGTCTTCTATGCTGCTGAGATCTGCTGTGGCCT 1048

Qy        912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 971
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Db       1049 GGAAGACCTGCACCGGGAACGCATTGTGTACAGGGATCTAAAGCCAGAGAATATCCTTCT 1108

Qy        972 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
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Db       1109 GGATGACCATGGCCACATTCGGATCTCGGACCTGGGACTGGCCGTGCATGTGCCTGAGGG 1168

Qy       1032 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1091
              | || ||||||      | |  || ||    || ||||||||||| ||| |  | | |
Db       1169 CCAGACCATCAAAGGCCGTGTGGGCACTGTGGGCTACATGGCTCCAGAGGTGGTGAGG-- 1226

Qy       1092 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1151
               || |   | ||  | |    |   |||||||  ||  | || |||  | | || || ||
Db       1227 -AATGAGCGCTACACGTTCAGTCCTGACTGGTGGGCGCTAGGCTGCCTCCTGTACGAGAT 1285

Qy       1152 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
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Db       1286 GATCGCAGGTCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATAAAGCGCGAAGAGGTGGA 1345

Qy       1212 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
              ||          | |||  |  |   | | |    |       | | || |||
Db       1346 GCGGCTGGTCAAGGAAGTGGCCGAGGAGTACACAGACCGCTTTTCCTCACAGGCGCGCTC 1405

Qy       1272 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331
              |     ||    |||  |        |     | ||||  |      |  |  |||
Db       1406 ACTCTGTTCTCAGCTTCTTAGCAAGGACCCTGCTGAGCGCCTGGGGTGTCGTGGAGGTGG 1465

Qy       1332 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1391
                |   |||    | | | || |   | || || |   | || ||    || |||| |||
Db       1466 CGCCCGTGAGGTAAAGGAGCACCCCCTTTTCAAGAAACTGAATTTCAAGCGGCTGGGAGC 1525

Qy       1392 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1451
              |||| |  | || || || |||  ||| || ||    |   |||||  ||| ||  ||
Db       1526 TGGCATGCTAGAGCCACCTTTTAAGCCTGATCCCCAGGCTATTTATTGCAAGGATGTCCT 1585

Qy       1452 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1511
               || |||||  | ||||||   |||   || |||||  | ||   || |||  |  | ||
Db       1586 GGACATTGAACAGTTCTCTACAGTTAAAGGTGTGGATCTGGAGCCCACAGACCAAGACTT 1645
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Qy       1512 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1571
              || | | || ||||| |||||   |||  | ||  | |||||| | || ||  | || ||
Db       1646 CTACCAGAAGTTTGCCACAGGCAGTGTGTCCATCCCCTGGCAGAATGAGATGGTGGAGAC 1705

Qy       1572 GGGACTGTTTGAGGAACTGAATGAC 1596
               |     ||  ||||||| |||| |
Db       1706 CGAGTGCTTCCAGGAACTCAATGTC 1730

RESULT 3
BX404586/c
LOCUS       BX404586                1201 bp    mRNA    linear   EST 13-MAY-2003
DEFINITION  BX404586 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
            CS0DA004YM05 3-PRIME, mRNA sequence.
ACCESSION   BX404586
VERSION     BX404586.1  GI:30648023
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 3090.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0AA004AG03NP1&cluster=3090.f. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0AA004AG03NP1.
FEATURES             Location/Qualifiers
     source          1..1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DA004YM05"
                     /tissue_type="NEUROBLASTOMA"
                     /clone_lib="Homo sapiens NEUROBLASTOMA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match             18.8%;  Score 311.8;  DB 13;  Length 1201;
  Best Local Similarity   59.8%;  Pred. No. 3.5e-60;
  Matches  539;  Conservative    1;  Mismatches  358;  Indels    3;  Gaps    1;

Qy        522 GTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTT 581
              :|| |||||||||||     | || | ||| |||||| |  | ||   |||||   | |
Db       1004 KTTCCTGCAGTGGAAGTGGCTGGAAARGCAGCCAGTGACCAAAAACACCTTCAAGCAATA 945

Qy        582 CAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGG 641
              | |||| ||||| |||||||| ||||||||||| || |||  |||||||     ||| ||
Db        944 CCGAGTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGG 885

Qy        642 GAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAA 701
               |||||||||||||| ||||| || || || |||||| | ||||||      || |||
Db        884 TAAGATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAGGC 825

Qy        702 GATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCT 761
               ||||| ||    || ||| | ||| ||||||| || | |||    ||  | ||     |
Db        824 CATGGCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTT 765
```

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Qy        762 GGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGG 821
              |||||| |||| ||||| ||||  |   || ||||| ||  |||  |||||||| |||||
Db        764 GGCCTACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGG 705

Qy        822 AGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGAT 881
               ||||||||||||||||||||| || |||||  |  |||| |   |      ||||   |
Db        704 CGACCTCAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGCCGT 645

Qy        882 CTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTA 941
              ||| ||| | ||| ||||   ||||||  ||  | |||| ||        ||||||| ||
Db        644 CTTCTACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTA 585

Qy        942 TCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGA 1001
                ||||| ||||||| |||||  |  | |||||||||| |||| ||  | |  | |||||
Db        584 CAGGGACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTCTGA 525

Qy       1002 CCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAA 1061
              |||||| || || ||| |  ||   |  ||| || ||||||    | | |  || |||
Db        524 CCTGGGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGT 465

Qy       1062 TGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTG 1121
               |||||||||||||| |||    |  || | || | | | ||  | |        |||||
Db        464 GGGTTACATGGCTCCGGAG---GTGGTGAAGAATGAACGGTACACGTTCAGCCCTGACTG 408

Qy       1122 GTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTA 1181
              ||  ||  | || |||  | | || || ||| | || || |   | || ||| |  |
Db        407 GTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCAGAG 348

Qy       1182 CAAGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATT 1241
               ||| | ||| |||     |||||  || |||          | | | |   |   | |
Db        347 GAAGAAGAAGATCAAGCGGGAGGAGGTGGAGCGGCTGGTGAAGGAGGTCCCCGAGGAGTA 288

Qy       1242 CCAGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAA 1301
                   |       | | |  |||       |  |   |    |||| |||      |
Db        287 TTCCGAGCGCTTTTCCCCGCAGGCCCGCTCACTTTGCTCACAGCTCCTCTGCAAGGACCC 228

Qy       1302 ACCAGAGCAACGCTTAGGAAGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTT 1361
                | || |  |      |  |  | |  |   |    ||    | | | || |   ||||
Db        227 TGCCGAACGCCTGGGGTGTCGTGGGGGCAGTGCCCGCGAGGTGAAGGAGCACCCCCTCTT 168

Qy       1362 TAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGA 1421
              ||| | | | |||||    || |||| ||||||| |  | || || || ||   ||| ||
Db        167 TAAGAAGCTGAACTTCAAGCGGCTGGGAGCTGGCATGCTGGAGCCGCCCTTCAAGCCTGA 108

Qy       1422 C 1422
              |
Db        107 C 107


RESULT 4
BC027597
LOCUS       BC027597               2329 bp    mRNA    linear   HTC 01-MAY-2002
DEFINITION  Homo sapiens, Similar to G protein-coupled receptor kinase 2-like
            (Drosophila), clone IMAGE:4830673, mRNA.
ACCESSION   BC027597
VERSION     BC027597.1  GI:20379554
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2329)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-APR-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) &  Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Institute for Systems Biology
            http://www.systemsbiology.org
            contact: amadan@systemsbiology.org
            Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha
            Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 34 Row: i Column: 14
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 4885346
            This clone has the following problem: frame shifted.
FEATURES             Location/Qualifiers
     source          1. .2329
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4830673"
                     /tissue_type="Testis"
                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
                     /note="Vector: pBluescript"
ORIGIN

  Query Match             18.8%;  Score 311.6;  DB 11;  Length 2329;
  Best Local Similarity   57.4%;  Pred. No. 5.5e-60;
  Matches  623;  Conservative    0;  Mismatches  454;  Indels    9;  Gaps    3;

Qy        477 AGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAA 536
              || | | || ||| | || | |      ||| | |  |      ||||| | || |||||
Db        921 AGGGGAACCATTTGAAGAATACCAAGAAAGCTCATATTTTTCTCAGTTTTTACAATGGAA 980

Qy        537 ACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAA 596
              |    | || | |||||| ||  || | ||    || |   | | ||||||| || || ||
Db        981 ATGGCTGGAAAGGCAACCCGTAACAAAGAACACATTTAGACATTACAGAGTTCTAGGAAA 1040

Qy        597 AGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTG 656
              ||| || ||||| ||||| || |||   || |||  |  ||| || || |||||||||||
Db       1041 AGGCGGATTTGGAGAGGTTTGCGCCTGTCAAGTGCGAGCCACAGGAAAAATGTATGCCTG 1100

Qy        657 TAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGA 716
               || || ||  | || ||  |  | |||||||     || ||    ||||||||    ||
Db       1101 CAAAAAGCTACAAAAAAAAAGAATAAAGAAGAGGAAAGGTGAAGCTATGGCTCTAAATGA 1160

Qy        717 AAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGA 776
               ||   |||  ||||||| ||    ||    ||| | ||   | | ||||| || | |||
Db       1161 GAAAAGAATTCTGGAGAAAGTGCAAAGTAGATTCGTAGTTAGTTTAGCCTACGCTTATGA 1220

Qy        777 GAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCA 836
               | |||        | ||| | ||  | | | | |||||||| || ||  | ||||| ||
Db       1221 AACCAAAGATGCCTTGTGCTTGGTGCTCACCATTATGAATGGAGGGGATTTGAAGTTTCA 1280

Qy        837 CATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCA 896
              ||| ||||||| ||||||  |  ||| | ||   |    | |   | || ||  | ||  |
Db       1281 CATTTACAACCTGGGCAATCCCGGCTTTGATGAGCAGAGAGCCGTTTTCTATGCTGCAGA 1340

Qy        897 GATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCC 956
              | |    || ||  ||    |  | ||        | || || ||  | ||| |||||||
Db       1341 GCTGTGTTGCGGCTTGGAAGATTTACAGAGGGAAAGAATTGTATACAGAGACTTGAAGCC 1400

Qy        957 TGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGT 1016
              ||||||| | || || ||||| |  ||  ||  | || | || ||||| ||  |||||
Db       1401 TGAGAATATTCTCCTTGATGATCGTGGACACATCCGGATTTCAGACCTCGGTTTGGCCAC 1460

Qy       1017 GGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCC 1076
               |||||    |  ||  ||    |        || | ||||||    || |||||||| ||
Db       1461 AGAGATCCCAGAAGGACAGAGGGTTCGAGGAAGAGTTGGAACAGTCGGCTACATGGCACC 1520

Qy       1077 TGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATG 1136
              |||  |  | |   | || | ||  ||| | | |  |   || ||||  |   | |  ||
Db       1521 TGAAGTTGTCA---ATAATGAAAAGTATACGTTTAGTCCCGATTGGTGGGGACTTGGCTG 1577
```

```
Qy       1137 CAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAG 1196
                  || ||||||||| ||   ||||   | ||||||||| | ||||| || || ||||
Db       1578 TCTGATCTATGAAATGATTCAGGGACATTCTCCATTCAAAAAATACAAAGAGAAAGTCAA 1637

Qy       1197 TAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTT 1256
                  |||||  |  | |||||||   |  |  | ||   | |     |   ||| || ||
Db       1638 ATGGGAGGAGGTCGATCAAAGAA---TCAAGAATGATACCGAGGAGTATTCTGAGAAGTT 1694

Qy       1257 CACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTT 1316
                ||||||| || |||  ||| |||||| | ||  |  | ||||| |||    | ||  |
Db       1695 TTCAGAGGATGCCAAATCTATCTGCAGGATGTTACTCACCAAGAATCCAAGCAAGCGGCT 1754

Qy       1317 AGGAAGCAGAGAAAAG---TCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAA 1373
               ||  |||| |   ||    | | ||     | | | || |   | || ||    |||||
Db       1755 GGGCTGCAGGGGCGAGGGAGCGGCTGGGGTGAAGCAGCACCCCGTGTTCAAGGACATCAA 1814

Qy       1374 CTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGT 1433
              |||     | ||||| ||   | |  | || ||||| ||    || || |||   |  ||
Db       1815 CTTCAGGAGGCTGGAGGCAAACATGCTGGAGCCCCCTTTCTGTCCTGATCCTCATGCCGT 1874

Qy       1434 TTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGA 1493
              |||    || ||| ||   || || ||  | ||||| | |||    ||| |  |  | ||
Db       1875 TTACTGTAAGGACGTCCTGGATATCGAGCAGTTCTCGGCGGTGAAAGGGATCTACCTGGA 1934

Qy       1494 TGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCA 1553
                 |  |||| |  | ||||        ||||| || ||   |||  | ||  | |||||
Db       1935 CACCGCAGATGAAGACTTCTATGCTCGGTTTGCTACCGGGTGTGTCTCCATCCCCTGGCA 1994

Qy       1554 GGAAGA 1559
              | | ||
Db       1995 GAATGA 2000


RESULT 5
BX392018/c
LOCUS       BX392018                 917 bp    mRNA    linear   EST 13-MAY-2003
DEFINITION  BX392018 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
            Homo sapiens cDNA clone CS0DL010YD11 3-PRIME, mRNA sequence.
ACCESSION   BX392018
VERSION     BX392018.1  GI:30607809
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 917)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 3090.f For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAI046ZH12_CS04416_1&cluster=3090.f.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAI046ZH12_CS04416_1.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DL010YD11"
                     /cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
                     /cell_line="RAMOS CELL LINE"
                     /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
                     25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             18.5%;  Score 307;  DB 13;  Length 917;
  Best Local Similarity   63.8%;  Pred. No. 3.7e-59;
  Matches  482;  Conservative    0;  Mismatches  270;  Indels    3;  Gaps    1;

Qy        459 GGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGA 518
              | ||    | | | ||   | |   || |||   || | | |   ||||  || || | |
Db        796 GACCCACGAGTACCTGAGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAA 737

Qy        519 CAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGA 578
              |   || |||||||||||     | || | ||| |||||| |  | ||   |||||   |
Db        736 CCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCA 677

Qy        579 GTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACAC 638
               | | |||| ||||| |||||||| ||||||||||| || |||  |||||||     |||
Db        676 ATACCGAGTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCAC 617

Qy        639 TGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGA 698
               || |||||||||||||| ||||| || || || |||||| | ||||||      || ||
Db        616 AGGTAAGATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGA 557

Qy        699 GAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTC 758
              |   ||||| ||    || ||| | ||| ||||||| || | |||    ||  | ||
Db        556 GGCCATGGCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAG 497

Qy        759 TCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGG 818
                ||||||| |||| ||||| ||||  |   || ||||| ||  |||  |||||||| ||
Db        496 CTTGGCCTACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGG 437

Qy        819 GGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGT 878
              ||| ||||||||||||||||||||| || |||||  |  |||| |   |      ||||
Db        436 GGGCGACCTCAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGC 377

Qy        879 GATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGT 938
                |||| ||| | ||| ||||   ||||||  ||  | |||| ||        |||||||
Db        376 CGTCTTCTACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGT 317

Qy        939 CTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATC 998
               ||  ||||| ||||||| |||||  |  | |||||||||| |||| ||  | |  | ||
Db        316 GTACAGGGACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTC 257

Qy        999 TGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAAC 1058
              ||||||||| || || ||| |  ||   |  ||| || ||||||    | | |  || ||
Db        256 TGACCTGGGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCAC 197

Qy       1059 CAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGA 1118
              |   |||||||||||||| |||    |  || | || | | | ||  | |        ||
Db        196 CGTGGGTTACATGGCTCCGGAG---GTGGTGAAGAATGAACGGTACACGTTCAGCCCTGA 140

Qy       1119 CTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGA 1178
              |||||  ||  | || |||  | | || || ||| | || || |   | || ||| |  |
Db        139 CTGGTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCA 80

Qy       1179 TTACAAGGAAAAGGTCAGTAAAGAGGATCTGAAGC 1213
                  ||| | ||| |||     |||||  || |||
Db         79 GAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGAGC 45


RESULT 6
AY406080
LOCUS       AY406080                1721 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Homo sapiens GPRK5 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY406080
VERSION     AY406080.1  GI:39762054
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1721)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1721)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1..>1721
                     /gene="GPRK5"
                     /locus_tag="HCM2438"
ORIGIN

  Query Match             18.4%;  Score 304.6;  DB 29;  Length 1721;
  Best Local Similarity   49.5%;  Pred. No. 1.9e-58;
  Matches  559;  Conservative    0;  Mismatches  561;  Indels    9;  Gaps    3;

Qy         469 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 528
               | | ||   |   | || ||  | || |   ||  ||||   || |  |||   |||||
Db         402 TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTTGACCGCTTTCTC 461

Qy         529 CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 588
               ||||||||    || || |
Db         462 CAGTGGAAGTGGTTGGAAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 521

Qy         589 CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG 648
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Db         522 NNNNNNNNNNNNNNNNNNNNNNNNGTCTGTGCCTGCCAGGTTCGGGCCACGGGTAAAATG 581

Qy         649 TATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCT 708
               |||||||| |||    |||| |||||| || | || ||||     || |||   |||||
Db         582 TATGCCTGCAAGCGCTTGGAGAAGAAGAGGATCAAAAAGAGGAAAGGGGAGTCCATGGCC 641

Qy         709 CTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTAT 768
               |||   || ||| | ||| | |||||||||| ||| |  ||  | |||   |||||||||
Db         642 CTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCCTAT 701

Qy         769 GCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTC 828
               ||||  |||| ||||      || ||| | ||| ||| | | ||||||||||| |||||
Db         702 GCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGACCTG 761

Qy         829 AAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTAC 888
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Db         762 AAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTTTAT 821

Qy         889 TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 948
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Qy         949 ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1008
                |||| ||||| ||  | ||  | |||||    ||| ||   ||| | || ||||||||
Db         882 CTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTGGGC 941

Qy        1009 CTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTAC 1068
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Db         942 TTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGCACTGTTGGCTAC 1001
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Qy        1069 ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1128
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Db        1002 ATGGCTCCAGAGGTCC---TGAACAACCAGAGGTACGGCCTGAGCCCCGACTACTGGGGC 1058

Qy        1129 ATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAA 1188
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Db        1059 CTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCAAGGAG 1118

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Db        1119 AAGGTGAAGCGGGAGGAGGTGGACCGCCGGGTCCTGGAGACGGAGGAGGTGTACTCCCAC 1178

Qy        1249 GATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAG 1308
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Db        1179 ---AAGTTCTCCGAGGAGGCCAAGTCCATCTGCAAGATGCTGCTCACGAAAGATGCGAAG 1235

Qy        1309 CAACGCTTAGGAAGCAGAGAAAA---GTCTGATGATCCCAGGAAACATCATTTCTTTAAA 1365
               ||  |  | ||  ||   ||  |   | |||  ||   || || ||| |  ||||| |
Db        1236 CAGAGGCTGGGCTGCCAGGAGGAGGGGGCTGCAGAGGTCAAGAGACACCCCTTCTTCAGG 1295

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Db        1296 AACATGAACTTCAAGCGCTTAGAAGCCGGGATGTTGGACCCTCCCTTCGTTCCAGACNNN 1355

Qy        1426 TCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTG 1485

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Qy        1486 GAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATA 1545

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Qy        1546 GCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATG 1594
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RESULT 7
BQ057469
LOCUS       BQ057469                1058 bp    mRNA    linear   EST 29-MAR-2002
DEFINITION  AGENCOURT_6739297 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5813090
            5', mRNA sequence.
ACCESSION   BQ057469
VERSION     BQ057469.1  GI:19816809
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1058)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2064  row: j  column: 03
            High quality sequence stop: 631.
FEATURES             Location/Qualifiers
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                     /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match             18.1%;  Score 300.2;  DB 13;  Length 1058;
  Best Local Similarity   63.9%;  Pred. No. 1.5e-57;
  Matches  471;  Conservative    0;  Mismatches  263;  Indels    3;  Gaps    1;

Qy      459 GGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGA 518
            | ||   |  | | ||   | |   || |||   || | | |   ||||  || || | |
Db        5 GACCCACGAGTACCTGAGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAA 64

Qy      519 CAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGA 578
            |   || |||||||||||     | || | ||| |||||| |  | ||   |||||   |
Db       65 CCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCA 124

Qy      579 GTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACAC 638
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Db      125 ATACCGAGTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCAC 184

Qy      639 TGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGA 698
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Db      185 AGGTAAGATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGA 244

Qy      699 GAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTC 758
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Db      245 GGCCATGGCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAG 304

Qy      759 TCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGG 818
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Db      305 CTTGGCCTACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGG 364

Qy      819 GGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGT 878
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Db      365 GGGCGACCTCAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGC 424

Qy      879 GATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGT 938
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Db      425 CGTCTTCTACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGT 484

Qy      939 CTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATC 998
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Db      485 GTACAGGGACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTC 544

Qy      999 TGACCTGGGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAAC 1058
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Qy     1059 CAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGA 1118
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Qy     1119 CTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGA 1178
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Db      662 CTGGTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAAGCCAGTCGCCCTTCCAGCA 721

Qy     1179 TTACAAGGAAAAGGTCA 1195
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Db      722 GAGGAAGAAGAAGATCA 738


RESULT 8
BQ061148
LOCUS       BQ061148                1019 bp    mRNA    linear   EST 02-APR-2002
DEFINITION  AGENCOURT_6862941 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920180
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            5', mRNA sequence.
ACCESSION   BQ061148
VERSION     BQ061148.1  GI:19884933
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2083  row: h  column: 05
            High quality sequence stop: 704.
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                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Size-selected >500bp for average insert size
                     1.8kb. Library constructed by Ling Hong in the laboratory
                     of Gerald M. Rubin (University of California, Berkeley)
                     using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                     II RT (Life Technologies). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match             18.0%;  Score 299.2;  DB 13;  Length 1019;
  Best Local Similarity   63.8%;  Pred. No. 2.4e-57;
  Matches  470;  Conservative    0;  Mismatches  264;  Indels    3;  Gaps    1;

Qy      459 GGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGA 518
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Db        5 GACCCACGAGTACCTGAGCGTGGCCCCTTTTGCCGACTACCTCGACAGCATCTACTTCAA 64

Qy      519 CAAGTTTCTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGA 578
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Db       65 CCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCA 124

Qy      579 GTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACAC 638
             | | |||| ||||| ||||||||| ||||||||||| || |||  |||||||     |||
Db      125 ATACCGAGTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCAC 184

Qy      639 TGGGAAGATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGA 698
             || |||||||||||||| ||||| || || || |||||| | ||||||      || ||
Db      185 AGGTAAGATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGA 244

Qy      699 GAAGATGGCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTC 758
            |   ||||| ||    || ||| | ||| |||||||| || | |||    ||  | ||
Db      245 GGCCATGGCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAG 304

Qy      759 TCTGGCCTATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGG 818
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Db      305 CTTGGCCTACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGG 364

Qy      819 GGGAGACCTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGT 878
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Db          365 GGGCGACCTCAAGTTCCACATCTACCACATGGGCCAGGCTGGCTTCCCCGAAGCGCGGGC 424

Qy          879 GATCTTTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGT 938
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Db          425 CGTCTTCTACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGT 484

Qy          939 CTATCGGGACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATC 998
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Db          485 GTACAGGGACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTC 544

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Qy         1059 CAATGGTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGA 1118
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Db          605 CGTGGGTTACATGGCTCCGGAG---GTGGTGAAGAATGAACGGTACACGTTCAGCCCTGA 661

Qy         1119 CTGGTTTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGA 1178
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Db          662 CTGGTGGGCGCTCGGCTGCCTCCTGTACGAGATGATCGCAGGCCAGTCGCCCTTCCAGCA 721

Qy         1179 TTACAAGGAAAAGGTCA 1195
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Db          722 GAGGAAGAAGAAAATCA 738


RESULT 9
AY406082
LOCUS       AY406082                1721 bp    DNA     linear   GSS 15-DEC-2003
DEFINITION  Mus musculus GPRK5 gene, VIRTUAL TRANSCRIPT, partial sequence,
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ACCESSION   AY406082
VERSION     AY406082.1  GI:39762056
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1721)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 1721)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence was made by sequencing genomic exons and ordering
            them based on alignment.
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     gene            <1..>1721
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ORIGIN

  Query Match             17.8%;  Score 295;  DB 29;  Length 1721;
  Best Local Similarity   49.0%;  Pred. No. 3e-56;
  Matches  553;  Conservative    0;  Mismatches  567;  Indels    9;  Gaps    3;

Qy          469 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 528
                | |||| | |   | |||||  | || | | ||   |||   |  |  |||   ||||||
Db          402 TACTTGAAGGGAGACCCCTTCCACGAGTACCTGGATAGCATGTATTTTGACCGTTTTCTG 461

Qy          529 CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 588
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Db          462 CAGTGGAAATGGTTAGAAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 521

Qy          589 CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG 648
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Db          522 NNNNNNNNNNNNNNNNNNNNNNNNGTCTGTGCCTGCCAGGTTCGGGCCACTGGTAAAATG 581

Qy          649 TATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCT 708
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Db          582 TATGCTTGTAAACGCTTAGAGAAGAAGAGGATCAAAAAGAGGAAAGGCGAATCCATGGCA 641

Qy          709 CTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTAT 768
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Db          642 CTCAACGAAAAGCAGATTCTTGAGAAGGTCAACAGCCAGTTTGTGGTCAACCTGGCCTAT 701

Qy          769 GCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTC 828
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Db          702 GCCTATGAAACCAAAGATGCACTATGCCTGGTTCTGACCATTATGAATGGTGGTGACCTG 761

Qy          829 AAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTAC 888
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Db          762 AAGTTTCACATCTACAATATGGGGAATCCTGGCTTTGAGGAAGAGCGAGCCTTATTTTAT 821

Qy          889 TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 948
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                ||||| || ||  | || |   |  ||  |  |         ||||   |||||   | |
Db         1002 ATGGCCCCAGAAGTTCTGAACAACCAGCGATATGGACTGAGCCCTGACTACTGG---GGC 1058

Qy         1129 ATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAA 1188
                 |||| |||  ||| ||||| ||| |||  || |   |||||||   || |  ||||||
Db         1059 CTGGGCTGCCTCATCTATGAGATGATTGAAGGCCAGTCACCATTTCGAGGTCGCAAGGAG 1118

Qy         1189 AAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCAT 1248
                ||||| |     || ||  || | |   |    ||| |    ||||   || |  |
Db         1119 AAGGTTAAGCGGGAAGAGGTGGATCGCCGGGTGCTGGAGACTGAGG---AAGTATATTCC 1175

Qy         1249 GATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAG 1308
                   || ||| | || || || ||    || ||||   |  |  |  | ||  |  |  ||
Db         1176 TCCAAGTTCTCTGAAGAGGCCAAGTCCATCTGCAACATGCTGCTCACCAAAGACTCGAAG 1235

Qy         1309 CAACGCTTAGGAAGCAGAGAAAA---GTCTGATGATCCCAGGAAACATCATTTCTTTAAA 1365
                ||  |  | ||  ||   ||  |   | | |  ||   || ||  || | |||||| |
Db         1236 CAGAGGCTGGGCTGCCAGGAGGAGGGGGCCGCCGAGGTCAAGAGGCACCCTTTCTTCAGG 1295

Qy         1366 ACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCT 1425
                |  || ||||||   |||||||| |||||  |  | || || || || || |||||
Db         1296 AACATGAACTTTAAGCGCCTGGAGGCTGGGATGTTGGACCCTCCCTTCGTTCCAGATNNN 1355

Qy         1426 TCAGTGGTTTATGCCAAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTG 1485

Db         1356 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1415

Qy         1486 GAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATA 1545

Db         1416 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 1475

Qy         1546 GCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATG 1594
                               || |||||||| | |   ||  |||| |||||||
Db       1476 NNNNNNNNNNNNNNNATGATAGAAACAGAATGTTTCAAGGAGCTGAATG 1524


RESULT 10
BU526699
LOCUS       BU526699                 934 bp    mRNA    linear   EST 13-SEP-2002
DEFINITION  AGENCOURT_10181837 NIH_MGC_101 Homo sapiens cDNA clone
            IMAGE:6536408 5', mRNA sequence.
ACCESSION   BU526699
VERSION     BU526699.1  GI:22837140
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 934)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2697  row: 1  column: 08
            High quality sequence stop: 640.
FEATURES             Location/Qualifiers
     source          1..934
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6536408"
                     /tissue_type="epidermoid carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_101"
                     /note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
                     XhoI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             17.0%;  Score 281.8;  DB 13;  Length 934;
  Best Local Similarity   62.6%;  Pred. No. 2.2e-53;
  Matches  455;  Conservative    0;  Mismatches  269;  Indels    3;  Gaps    1;

Qy         469 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 528
               | | ||   |   | || ||  | || |   ||  ||||   || |  |||   |||||
Db          78 TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTTGACCGCTTTCTC 137

Qy         529 CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 588
               ||||||||    || || | |||||| ||| |  | ||    ||||   |||   |||||
Db         138 CAGTGGAAGTGGTTGGAAAGGCAACCGGTGACCAAAAACACTTTCAGGCAGTATCGAGTG 197

Qy         589 CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG 648
               || || ||||| || || |||||||| ||||||  ||||||      ||| || || |||
Db         198 CTAGGAAAAGGGGGCTTCGGGGAGGTCTGTGCCTGCCAGGTTCGGGCCACGGGTAAAATG 257

Qy         649 TATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCT 708
               |||||||| |||    |||| |||||| || | || ||||     || |||   |||||
Db         258 TATGCCTGCAAGCGCTTGGAGAAGAAGAGGATCAAAAAGAGGAAAGGGGAGTCCATGGCC 317

Qy         709 CTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTAT 768
               |||   || ||| | ||| | |||||||||| ||| |  ||  | |||   |||||||||
Db         318 CTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCCTAT 377

Qy         769 GCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTC 828
               ||||  |||| ||||      || ||| | ||| ||| | | ||||||||||| |||||
Db         378 GCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGACCTG 437

Qy         829 AAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTAC 888
               |||||||||||||||||| ||||||  | |||| | ||   |   ||||   | |||||
Db         438 AAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTTTAT 497

Qy         889 TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 948
                ||||  ||||   ||| ||  |     |||||||         || |||||| || ||
Db         498 GCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGAGAT 557

Qy         949 ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1008
                |||| ||||| ||  | ||  | |||||    ||| ||   ||| | || ||||||||
Db         558 CTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTGGGC 617

Qy        1009 CTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTAC 1068
                |||| ||| ||||    |  ||  | |  |||  |    |||  || ||   ||| |||
Db         618 TTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGNCGGGTGGGCACTGTTGGCTAC 677

Qy        1069 ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1128
               |||||||| ||| |||   || || |    || ||   |         ||||  |  | |
Db         678 ATGGCTCCAGAGGTCC---TGAAACACCAGAGGTACGGCCTGAGCCCCGACTACTGGGGC 734

Qy        1129 ATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAA 1188
                | || |||  ||| ||||| ||| | |  || |   | || |||   |    ||||||
Db         735 CTTGGCTGCCTCATCTATGAGATGATCGAAGGCCAGTCGCCGTTCCGCGGNCGCAAGGAG 794

Qy        1189 AAGGTCA 1195
               || || |
Db         795 AAAGTGA 801


RESULT 11
BU146436
LOCUS       BU146436                 903 bp    mRNA    linear   EST 03-SEP-2002
DEFINITION  AGENCOURT_8728162 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:6339126
            5', mRNA sequence.
ACCESSION   BU146436
VERSION     BU146436.1  GI:22659968
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 903)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2533  row: h  column: 07
            High quality sequence stop: 635.
FEATURES             Location/Qualifiers
     source          1..903
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6339126"
                     /tissue_type="neuroblastoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_47"
                     /note="Organ: brain; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
```

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                  insert size 1.8kb.  Library constructed by Ling Hong in
                  the laboratory of Gerald M. Rubin (University of
                  California, Berkeley) using ZAP-cDNA synthesis kit
                  (Stratagene) and Superscript II RT (Life Technologies).
                  Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             16.9%;  Score 280.6;  DB 13;  Length 903;
  Best Local Similarity   62.6%;  Pred. No. 4.1e-53;
  Matches  455;  Conservative    0;  Mismatches  269;  Indels    3;  Gaps    1;

Qy        469 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 528
              | | ||   |   | || ||  | || |   ||  ||||   || |  |||   |||||
Db         93 TACCTGAGGGGAGAACCATTCCACGAATATCTGGACAGCATGTTTTTGACCGCTTTCTC 152

Qy        529 CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 588
              ||||||||    || || | |||||| ||| |  | ||    ||||   |||   |||||
Db        153 CAGTGGAAGTGGTTGGAAAGGCAACCGGTGACCAAAAACACTTTCAGGCAGTATCGAGTG 212

Qy        589 CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG 648
              || || ||||| || || |||||||| ||||||  ||||||      ||| || || |||
Db        213 CTAGGAAAAGGGGGCTTCGGGGAGGTCTGTGCCTGCCAGGTTCGGGCCACGGGTAAAATG 272

Qy        649 TATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCT 708
              |||||||| |||    |||| |||||| || | || ||||     || |||   |||||
Db        273 TATGCCTGCAAGCGCTTGGAGAAGAAGAGGATCAAAAAGAGGAAAGGGGAGTCCATGGCC 332

Qy        709 CTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTAT 768
              |||   || ||| | ||| | |||||||||| ||| |  ||  | |||   |||||||||
Db        333 CTCAATGAGAAGCAGATCCTCGAGAAGGTCAACAGTCAGTTTGTGGTCAACCTGGCCTAT 392

Qy        769 GCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGAGACCTC 828
              ||||  |||| ||||      || ||| | ||| ||| | | ||||||||||| |||||
Db        393 GCCTACGAGACCAAGGATGCACTGTGCTTGGTCCTGACCATCATGAATGGGGGTGACCTG 452

Qy        829 AAGTTCCACATCTACAACGTGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTAC 888
              |||||||||||||||||| ||||||  | |||| | ||   |   ||||   | |||||
Db        453 AAGTTCCACATCTACAACATGGGCAACCCTGGCTTCGAGGAGGAGCGGGCCTTGTTTTAT 512

Qy        889 TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 948
               ||||  ||||   ||| ||  |     |||||||         || |||||| || ||
Db        513 GCGGCAGAGATCCTCTGCGGCTTAGAAGACCTCCACCGTGAGAACACCGTCTACCGAGAT 572

Qy        949 ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1008
               |||| ||||| ||  | ||  | |||||    ||| ||   ||| | || ||||||||
Db        573 CTGAAACCTGAAAACATCCTGTTAGATGATTATGGCCACATTAGGATCTCAGACCTGGGC 632

Qy       1009 CTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTAC 1068
               |||| ||| ||||    |  ||  | |  |||  |    |||  || ||   ||| |||
Db        633 TTGGCTGTGAAGATCCCCGAGGGAGACCTGATCCGCGGCCGGGTGGGCACTGTTGGCTAC 692

Qy       1069 ATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCC 1128
              |||||||| ||| |||   || | ||    || ||   |         ||||  |  | |
Db        693 ATGGCTCCAGAGGTCC---TGAACAACCAGAGGTACGGCCTGAGCCCCGACTACTGGGGC 749

Qy       1129 ATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAA 1188
               | || |||  ||| ||||| ||| | |  || |   | || |||   |    ||||||
Db        750 CTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCAAGGAG 809

Qy       1189 AAGGTCA 1195
              || || |
Db        810 AAAGTGA 816


RESULT 12
BM794145
LOCUS       BM794145                 560 bp    mRNA    linear   EST 05-MAR-2002
DEFINITION  K-EST0075316 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-37-D08
            5', mRNA sequence.
ACCESSION   BM794145
VERSION     BM794145.1  GI:19142377
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 560)
  AUTHORS   Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
            Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
            Kim,Y.S.
  TITLE     21C Frontier Korean EST Project 2001
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 37  row: D  column: 08
            High quality sequence stop: 560.
FEATURES             Location/Qualifiers
     source          1..560
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S22SNU16n1-37-D08"
                     /sex="F"
                     /tissue_type="Ascites"
                     /cell_type="Lymphoblast-like"
                     /cell_line="SNU-16"
                     /lab_host="DH10B"
                     /clone_lib="S22SNU16n1"
                     /note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
                     Site_2: NotI; The S22SNU16 library was contributed by the
                     Soares laboratory and it was constructed as described by
                     Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
                     Research 6(9): 791-806. RNA was prepared from harvested
                     cells of SNU-16 culture. SNU-16 cell was obtained from
                     Korean Cell Line Bank (KCLB). SNU-16 was established from
                     ascitic fluids of Korean patients by Park J.G. et al.
                     (1990), Cancer Res 50: 2773-2780."
ORIGIN

  Query Match             16.4%;  Score 272.2;  DB 12;  Length 560;
  Best Local Similarity   68.0%;  Pred. No. 2.6e-51;
  Matches  379;  Conservative    0;  Mismatches  178;  Indels    0;  Gaps    0;

Qy        526 CTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGA 585
              |||||||||||     | || | ||| |||||| |  | ||   |||||   | | | ||
Db          1 CTGCAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCAATACCGA 60

Qy        586 GTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAG 645
              || ||||| |||||||| ||||||||||| || |||  |||||||     ||| || |||
Db         61 GTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAG 120

Qy        646 ATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATG 705
              ||||||||||| ||||| || || || |||||| | ||||||      || |||   |||
Db        121 ATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATG 180

Qy        706 GCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCC 765
              || ||    || ||| | ||| ||||||| || | |||    ||  | ||     |||||
Db        181 GCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCC 240

Qy        766 TATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGAGAC 825
              || |||| ||||| ||||  |   || ||||| ||  |||  |||||||| ||||| |||
Db        241 TACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGGCGAC 300

Qy        826 CTCAAGTTCCACATCTACAACGTGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTT 885
              |||||||||||||||||| || |||||  |  |||| |   |      ||||   ||||
Db        301 CTCAAGTTCCACATCTACCACATGGCCAGGCTGGCTTCCCCGAAGCGCGGCCGTCTTC 360

Qy        886 TACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGG 945
              ||| | ||| ||||   ||||||  ||  | |||| ||        /////// //  //
Db        361 TACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTACAGG 420
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Qy        946 GACATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTG 1005
              ||| ||||||| |||||  |  | |||||||||| |||| ||  | |  | |||||||||
Db        421 GACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGCCACATCCGCATCTCTGACCTG 480

Qy       1006 GGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGT 1065
              || || || ||| |  ||   |  ||| || ||||||    | | |  || |||   |||
Db        481 GGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGGGGGT 540

Qy       1066 TACATGGCTCCTGAGAT 1082
              ||||||||||| ||| |
Db        541 TACATGGCTCCGGAGGT 557

RESULT 13
BM697499
LOCUS       BM697499                 601 bp    mRNA    linear   EST 28-FEB-2002
DEFINITION  UI-E-DX0-agn-o-23-0-UI.r1 UI-E-DX0 Homo sapiens cDNA clone
            UI-E-DX0-agn-o-23-0-UI 5', mRNA sequence.
ACCESSION   BM697499
VERSION     BM697499.1  GI:19010757
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 601)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Soares, MB
            Coordinated Laboratory for Computational Genomics
            University of Iowa
            375 Newton Road , 4156  MEBRF, Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: bento-soares@uiowa.edu
            Tissue Procurement: Dr. Gregg Hageman
             cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
             Clone Distribution: Researchers may obtain clones from Research
            Genetics (www.resgen.com).
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .601
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-E-DX0-agn-o-23-0-UI"
                     /tissue_type="fetal eyes"
                     /dev_stage="fetal"
                     /lab_host="DH10B (Life Technologies) (T1 phage resistant)"
                     /clone_lib="UI-E-DX0"
                     /note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     UI-E-DX0 is a cDNA library containing the following
                     tissue(s): fetal eyes. The library was constructed
                     according to Bonaldo, Lennon and Soares, Genome Research,
                     6:791-806, 1996. First strand cDNA synthesis was primed
                     with an oligo-dT primer containing a Not I site. Double
                     stranded cDNA was ligated to an EcoR I adaptor, digested
                     with Not I, and cloned directionally into pT7T3-Pac
                     vector. The oligonucleotide used to prime the synthesis of
                     first-strand cDNA contains a library tag sequence that is
                     located between the Not I site and the (dT)18 tail. The
                     sequence tag for this library is AGAATCAAGA. This library
                     was created for the program, Gene Discovery in the Visual
                     System, supported by National Eye Institute (NEI)."
ORIGIN

  Query Match             16.4%;  Score 272.2;  DB 12;  Length 601;
  Best Local Similarity   67.5%;  Pred. No. 2.7e-51;
  Matches  382;  Conservative    0;  Mismatches  184;  Indels    0;  Gaps    0;

Qy        526 CTGCAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGA 585
              |||||||||||     | || | ||| |||||| |  | ||   |||||   | | | ||
Db          1 CTGCAGTGGAAGTGGCTGGAAAGGCAGCCAGTGACCAAAAACACCTTCAGGCAATACCGA 60

Qy        586 GTGCTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAG 645
              || ||||| |||||||| ||||||||||| || |||  |||||||     ||| || |||
Db         61 GTCCTGGGCAAAGGTGGCTTTGGGGAGGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAG 120

Qy        646 ATGTATGCCTGTAAGAAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATG 705
              ||||||||||| ||||| || || || |||||| | ||||||      || |||   |||
Db        121 ATGTATGCCTGCAAGAAGCTAGAGAAAAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATG 180

Qy        706 GCTCTCTTGGAAAAGGAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCC 765
              || ||    || ||| | ||| ||||||| || | |||    ||  | ||     |||||
Db        181 GCGCTGAACGAGAAGCAGATCCTGGAGAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCC 240

Qy        766 TATGCCTTTGAGAGCAAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGAC 825
              || |||| ||||| ||||  |   || ||||| ||  |||  |||||||| ||||| |||
Db        241 TACGCCTATGAGACCAAGGACGCGCTGTGCCTGGTGCTGACACTGATGAACGGGGGCGAC 300

Qy        826 CTCAAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTT 885
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Db        361 TACGCCGCCGAGATCTGCTGTGGCCTGGAGGACCTGCACCGGGAGCGCATCGTGTACAGG 420

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Db        421 GACCTGAAGCCCGAGAACATCTTGCTGGATGACCACGGNCACATCCGCATCTCTGACCTG 480

Qy       1006 GGGCTGGCCGTGGAGATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGT 1065
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Db        481 GGACTAGCTGTGCATGTGCCCGAGGGCCAGACCATCAAAGGGCGTGTGGGCACCGTGGGT 540

Qy       1066 TACATGGCTCCTGAGATCCTAATGGA 1091
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RESULT 14
BQ061150
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DEFINITION  AGENCOURT_6862973 NIH_MGC_99 Homo sapiens cDNA clone IMAGE:5920182
            5', mRNA sequence.
ACCESSION   BQ061150
VERSION     BQ061150.1  GI:19884936
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1017)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Lou Staudt
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2083  row: h  column: 07
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                  /note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
                  EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                  into EcoRI/XhoI sites using the following 5' adaptor:
                  GGCACGAG(G). Size-selected >500bp for average insert size
                  1.8kb. Library constructed by Ling Hong in the laboratory
                  of Gerald M. Rubin (University of California, Berkeley)
                  using ZAP-cDNA synthesis kit (Stratagene) and Superscript
                  II RT (Life Technologies). Note: this is a NIH_MGC
                  Library."
ORIGIN

  Query Match             16.4%;  Score 272.2;  DB 13;  Length 1017;
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Qy          884 TTTACTCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATC 943
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Qy         1064 GTTACATGGCTCCTGAGATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGT 1123
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Db          361 GCTACATGGCTCCAGAGGTCC---TGAACAACCAGAGGTACGGCCTGAGCCCCGACTACT 417

Qy         1124 TTGCCATGGGATGCAGCATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACA 1183
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Db          418 GGGGCCTTGGCTGCCTCATCTATGAGATGATCGAGGGCCAGTCGCCGTTCCGCGGCCGCA 477

Qy         1184 AGGAAAAGGTCAGTAAAGAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCC 1243
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Qy         1244 AGCATGATAACTTCACAGAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAAC 1303
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Db          595 CGAAGCAGAGGCTGGGCTGCCAGGAGGAGGGGGCTGCAGAGGTCAAGAGACACCCCTTCT 654

Qy         1361 TTAAAACGATCAACTTTCCTCGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAG 1420
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Qy         1481 GGGTGGAATTTGATGACAAAGATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTC 1540
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Qy         1541 CTATAGCATGGCAGGAAGAAATTATAGAAACGGGACTGTTTGAGGAACTGAATG 1594
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RESULT 15
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DEFINITION  wd17a07.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
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            KINASE GRK5 (HUMAN);, mRNA sequence.
ACCESSION   AI934968
VERSION     AI934968.1  GI:5673838
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REFERENCE   1  (bases 1 to 815)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
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            Seq primer: -40UP from Gibco
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                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR-amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match             16.3%;  Score 270.6;  DB 9;  Length 815;
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  Matches  439;  Conservative    0;  Mismatches  263;  Indels    3;  Gaps    1;

Qy          469 TTCTTGCAAGAGCAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTG 528
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Db          711 TACTTGAGGGGAGAACCATCCCACGAATATCTGGACAGCATGTTTTTNGACCGCTTTCTC 652

Qy          529 CAGTGGAAACTCTTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTG 588
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Qy          589 CTGGGGAAAGGTGGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATG 648
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Qy         829 AAGTTCCACATCTACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTAC 888
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Qy         889 TCGGCCCAGATAGCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGAC 948
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Qy         949 ATGAAGCCTGAGAATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGG 1008
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             Copyright (c) 1993 - 2004  Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:          August 13, 2004, 13:15:49 ; Search time 86.4555 Seconds
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Scoring table:   IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched:        682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:       1365418

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Post-processing: Minimum Match 0%
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    2 1655.4  99.8   1662  4 US-09-802-117-1             Sequence 1, Appli
    3 1654.2  99.7   1662  4 US-09-738-894A-1            Sequence 1, Appli
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    5 1046.8  63.1   1062  4 US-09-802-117-3             Sequence 3, Appli
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    8  419.8  25.3   2848  3 US-08-464-954A-2            Sequence 2, Appli
    9  418.2  25.2   2204  1 US-08-221-817-12            Sequence 12, Appl
   10  418.2  25.2   2204  1 US-08-454-439-12            Sequence 12, Appl
   11  418.2  25.2   2204  5 PCT-US94-10487-12           Sequence 12, Appl
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   28  251.6  15.2   1420  4 US-09-614-748A-11           Sequence 11, Appl
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                                 ALIGNMENTS

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; Patent No. 6444456
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/09/802,117
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER: US 60/188,449
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 2249
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-802-117-5

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        834 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 893

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        894 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 953

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        954 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 1013

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1014 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 1073

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1074 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 1133

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1134 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 1193

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1194 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 1253

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1254 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 1313

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1314 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1373

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1374 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1433

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1434 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1493

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1494 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1553

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1554 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1613

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1614 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1673

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1674 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1733

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1734 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1793

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1794 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1853

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1854 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1913

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1914 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1973

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1974 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 2012


RESULT 2
US-09-802-117-1
; Sequence 1, Application US/09802117
; Patent No. 6444456
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/09/802,117
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER: US 60/188,449
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-802-117-1

  Query Match             99.8%;  Score 1655.4;  DB 4;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1656;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGAYAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
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              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659


RESULT 3
US-09-738-894A-1
; Sequence 1, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636
;  CURRENT APPLICATION NUMBER: US/09/738,894A
;  CURRENT FILING DATE:  2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Human
US-09-738-894A-1

  Query Match             99.7%;  Score 1654.2;  DB 4;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1656;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
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RESULT 4
US-09-964-469-1
; Sequence 1, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV
;  CURRENT APPLICATION NUMBER: US/09/964,469
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 1662
;   TYPE: DNA
;   ORGANISM: Human
US-09-964-469-1

  Query Match             99.7%;  Score 1654.2;  DB 4;  Length 1662;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches 1656;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy      . 181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
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Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAG 1080

Qy       1081 ATCCTAATGGAAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATCCTAATGGGAAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGC 1140

Qy       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 ATTTATGAAATGGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAA 1200

Qy       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 GAGGATCTGAAGCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACA 1260

Qy       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGAAGCAAAAGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGA 1320

Qy       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 AGCAGAGAAAAGTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCT 1380

Qy       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 CGCCTGGAAGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCC 1440

Qy       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 AAAGACATCGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAA 1500

Qy       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATAAGCAGTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAA 1560

Qy       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1561 ATTATAGAAACGGGACTGTTTGAGGAACTGAATGACCCCAACAGACCTACGGGTTGTGAG 1620

Qy       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659
              |||||||||||||||||||||||||||||||||||||||
Db       1621 GAGGGTAATTCATCCAAGTCTGGCGTGTGTTTGTTATTG 1659


RESULT 5
US-09-802-117-3
; Sequence 3, Application US/09802117
; Patent No. 6444456
; GENERAL INFORMATION:
;  APPLICANT: Walke, D. Wade
;  APPLICANT:  Wilganowski, Nathaniel L.
;  APPLICANT:  Turner, C. Alexander Jr.
;  TITLE OF INVENTION: No. 6444456el Human G-Coupled Protein Receptor Kinases and Polynuc
;  TITLE OF INVENTION:  Encoding the Same
;  FILE REFERENCE: LEX-0147-USA
;  CURRENT APPLICATION NUMBER: US/09/802,117
;  CURRENT FILING DATE:  2001-03-08
;  PRIOR APPLICATION NUMBER: US 60/188,449
;  PRIOR FILING DATE: 2000-03-10
;  NUMBER OF SEQ ID NOS: 5
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 1062
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-09-802-117-3

  Query Match             63.1%;  Score 1046.8;  DB 4;  Length 1062;
  Best Local Similarity   99.8%;  Pred. No. 5.3e-249;
  Matches 1048;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60

Qy         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120

Qy        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180

Qy        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240

Qy        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db        421 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAG 660

Qy        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 AAACTGGACAAGAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAG 720

Qy        721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780
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Db          721 GAAATCTTGGAGAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGC 780

Qy          781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          781 AAGACCCATCTCTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATC 840

Qy          841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          841 TACAACGTGGGCACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATA 900

Qy          901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          901 GCCTGTGGGATGCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAG 960

Qy          961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          961 AATGTGCTTCTGGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAG 1020

Qy         1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1050
                ||||||||||||||||||||||||||||||
Db         1021 ATGAAGGGTGGCAAGCCCATCACCCAGAGG 1050


RESULT 6
US-09-738-894A-3
; Sequence 3, Application US/09738894A
; Patent No. 6331423
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636
;  CURRENT APPLICATION NUMBER: US/09/738,894A
;  CURRENT FILING DATE:  2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 36651
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(36651)
;   OTHER INFORMATION: n = A,T,C or G
US-09-738-894A-3

  Query Match             37.2%;  Score 617.4;  DB 4;  Length 36651;
  Best Local Similarity   96.8%;  Pred. No. 2.2e-142;
  Matches  630;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy            1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2076 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 2135

Qy           61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2136 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 2195

Qy          121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2196 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 2255

Qy          181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2256 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 2315

Qy          241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2316 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 2375

Qy          301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2376 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 2435

Qy          361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2436 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 2495

Qy          421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
                |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db         2496 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 2555

Qy          481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2556 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 2615

Qy          541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2616 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 2675

Qy          601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTAT 651
                ||||||||||||||| ||| |  ||||  |  |  |     |  || | ||
Db         2676 GGTTTTGGGGAGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCAT 2726


RESULT 7
US-09-964-469-3
; Sequence 3, Application US/09964469
; Patent No. 6579709
; GENERAL INFORMATION:
;  APPLICANT: GUEGLER, Karl et al
;  TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
;  TITLE OF INVENTION:  ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: CL000636DIV
;  CURRENT APPLICATION NUMBER: US/09/964,469
;  CURRENT FILING DATE:  2001-09-28
;  PRIOR APPLICATION NUMBER: 60/208,331
;  PRIOR FILING DATE: 2000-06-01
;  PRIOR APPLICATION NUMBER: 09/738,894
;  PRIOR FILING DATE: 2000-12-18
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 36651
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(36651)
;   OTHER INFORMATION: n = A,T,C or G
US-09-964-469-3

  Query Match             37.2%;  Score 617.4;  DB 4;  Length 36651;
  Best Local Similarity   96.8%;  Pred. No. 2.2e-142;
  Matches  630;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy            1 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2076 ATGGTGGACATGGGGGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGG 2135

Qy           61 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2136 AAGCCCTCGGACTGCGACAGCAAAGAGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCC 2195

Qy          121 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2196 GGGCTGCAGGGCTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGT 2255

Qy          181 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         2256 GAGCAGCAGCCCATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTC 2315

Qy          241 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 300
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2316 CGCAAGGCGGCAACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCC 2375

Qy        301 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2376 ACCAAAGACAGCGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGG 2435

Qy        361 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2436 AACCCGCAACCCTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAG 2495

Qy        421 GAAGAGCGAGTGGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 480
              |||||||||||||||||||||||||||  |||||||||||||||||||||||||||||||
Db       2496 GAAGAGCGAGTGGCTGCAGTGACGCTGGCCAAGGCTGAGGCCATGGCTTTCTTGCAAGAG 2555

Qy        481 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2556 CAGCCCTTTAAGGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTC 2615

Qy        541 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2616 TTCGAGATGCAACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGT 2675

Qy        601 GGTTTTGGGGAGGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTAT 651
              ||||||||||||||| ||| |  ||||  |  |  |     |  || | ||
Db       2676 GGTTTTGGGGAGGTAAGTGTCTCCCAGTAGCCAGGCTAGAAGGTGAAGCAT 2726


RESULT 8
US-08-464-954A-2
; Sequence 2, Application US/08464954A
; Patent No. 6255069
;  GENERAL INFORMATION:
;    APPLICANT:  BENOVIC, JEFFREY L.; GOMEZ, JORGE; KUNAPULI,
;    APPLICANT:  PRIYA
;    TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR
;    TITLE OF INVENTION:  MODULATING THE ACTIVITY OF G PROTEIN-COUPLED RECEPTOR
;    TITLE OF INVENTION:  KINASES GRK5 AND GRK6
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jane Massey Licata, Esq.
;      STREET:  Woodland Falls Corporate Park
;      STREET:  210 Lake Drive East, Suite 201
;      CITY:  Cherry Hill
;      STATE:  NJ
;      COUNTRY:  USA
;      ZIP:  08002
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/464,954A
;      FILING DATE:  Herewith
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/076,084
;      FILING DATE:  June 11, 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jane Massey Licata
;      REGISTRATION NUMBER:  32,257
;      REFERENCE/DOCKET NUMBER:  JEFF-0118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (609) 779-2400
;      TELEFAX:  (609) 779-8488
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2848
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    ANTI-SENSE:  NO
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US-08-464-954A-2

  Query Match             25.3%;  Score 419.8;  DB 3;  Length 2848;
  Best Local Similarity   56.2%;  Pred. No. 4.8e-94;
  Matches  891;  Conservative    0;  Mismatches  682;  Indels   12;  Gaps    5;

Qy         15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74
              ||  || || ||| |  | || ||||| |     ||  |||||||| |       |   |
Db         65 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 124

Qy         75 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
                |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db        125 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 184

Qy        132 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 191
               ||||  ||||| || |  |  ||    |   |||  ||||||||||| |||| |||  |
Db        185 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACGC 244

Qy        192 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 251
              ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db        245 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 304

Qy        252 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 311
                ||||||| || |  |||    | |  ||  || ||  ||| |        || |   |
Db        305 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 364

Qy        312 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 371
               | || ||| |   |   |   | || |  |||   | | |  || |    |   |
Db        365 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 421

Qy        372 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                ||| | | |||   ||| | | |  |  || ||| ||     | | |     || |
Db        422 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 480

Qy        432 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 491
                ||            | |  ||||||  ||   |  | | ||   | |   || |||
Db        481 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 538

Qy        492 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
               || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db        539 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 598

Qy        552 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
               |||||| |  | ||   |||||   | | | |||| ||||| |||||||| ||||||||
Db        599 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 658

Qy        612 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
              ||| || |||  |||||||     ||| || |||||||||||||| ||||| || || ||
Db        659 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 718

Qy        672 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 731
               |||||| | ||||||      || |||   ||||| ||    || ||| | ||| ||||
Db        719 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 778

Qy        732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 791
              ||| || | |||    ||  | ||     ||||||| |||| ||||| ||||  |   ||
Db        779 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTATGAGACCAAGGACGCGCT 838

Qy        792 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 851
               ||||| ||  |||  |||||||| ||||| ||||||||||||||||||||| || ||||
Db        839 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 898

Qy        852 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 911
              |  |  |||| |   |      ||||   |||| ||| | ||| ||||   ||||||  |
Db        899 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 958

Qy        912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 971
              |  | |||| ||        ||||||| ||  ||||| ||||||| |||||  |  | ||
Db        959 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 1018

Qy        972 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
              |||||||| |||| ||  | |  | ||||||||||| || || ||| |  ||   |  ||
Db       1019 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1078
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Qy       1032 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1091
              | || ||||||    | | |  || |||   ||||||||||||||| |||    |  || |
Db       1079 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1135

Qy       1092 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1151
               || | | | ||  | |        |||||||  ||  | || |||  | | || || ||
Db       1136 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1195

Qy       1152 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
              | |  | || |   | || ||| |  |    ||| | ||| |||     |||||  || |
Db       1196 GATCACAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1255

Qy       1212 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
              ||          | | | |   |   | |      |        | | |  |||
Db       1256 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGGTTTTCCCCGCAGGCCCGCTC 1315

Qy       1272 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331
              |  |   |    |||| |||      |     | || |  |      |  |  | |  |
Db       1316 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGCCTGGGGTGTCGTGGGGGCAG 1375

Qy       1332 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1391
                |    ||    | | | || |   |||||||| | | | |||||    || |||| |||
Db       1376 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1435

Qy       1392 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1451
              |||| |  | || || || ||   ||| |||||    |   ||||   ||| ||  |
Db       1436 TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGTTCT 1495

Qy       1452 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1511
               || |||||  | ||||||  |||   ||| |||||  | ||    |  ||  |||||||
Db       1496 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGCAGTT 1555

Qy       1512 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1571
              || | | || ||||| |||||   ||| || ||  | |||||| | || ||  | || ||
Db       1556 CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1615

Qy       1572 GGGACTGTTTGAGGAACTGAATGAC 1596
               |     ||  | || ||||||| |
Db       1616 CGAGTGCTTCCAAGAGCTGAATGTC 1640

RESULT 9
US-08-221-817-12
; Sequence 12, Application US/08221817
; Patent No. 5532151
;  GENERAL INFORMATION:
;    APPLICANT:  Chantry, David
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Hoekstra, Merle F.
;    TITLE OF INVENTION:  A No. 5532151el G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,817
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/123,932
;      FILING DATE:  17 SEP 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5532151and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31981
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2204 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  31..1758
US-08-221-817-12

  Query Match             25.2%;  Score 418.2;  DB 1;  Length 2204;
  Best Local Similarity   56.2%;  Pred. No. 1.1e-93;
  Matches  890;  Conservative    0;  Mismatches  683;  Indels   12;  Gaps    5;

Qy         15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74
              ||  || || ||| |  | || ||||| |     ||  |||||| |       |   |
Db         33 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 92

Qy         75 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
                |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db         93 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 152

Qy        132 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 191
               ||||  ||||| || |  |  ||    |   |||  |||||||||||| |||| ||| |
Db        153 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACCG 212

Qy        192 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 251
              ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db        213 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 272

Qy        252 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 311
                ||||||| || |  |||    | |  ||  || ||  ||| |        || |   |
Db        273 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 332

Qy        312 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 371
               | || ||| |   |   |   | || ||||   | | |  ||  |   |   |
Db        333 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 389

Qy        372 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                ||| | | |||   ||| | | |  |  || ||| ||     | | |     || |
Db        390 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 448

Qy        432 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 491
                ||            | |  ||||||  ||   |  | | ||   | |   || |||
Db        449 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 506

Qy        492 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
               || | | |   ||||  ||  || | ||   || |||||||||||     | || | |||
Db        507 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 566

Qy        552 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
               |||||| |  | ||   ||||||   | | | |||| ||||| |||||||| ||||||||
Db        567 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGTAAAGGTGGCTTTGGGGA 626

Qy        612 GGTATGTGCCGTCCAGGTGAAAAACACTGGAAAGATGTATGCCTGTAAGAAACTGGACAA 671
              ||| || |||  |||||||     ||| || |||||||||||||| |||||| || || ||
Db        627 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 686

Qy        672 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 731
               |||||| | ||||||      || |||   ||||| ||    || |||  | ||| ||||
Db        687 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 746

Qy        732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 791
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              ||| || | |||    ||  | ||     ||||||| |||| ||||| ||||  |   ||
Db        747 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTATGAGACCAAGGACGCGCT 806

Qy        792 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 851
               ||||| ||  |||  |||||||| ||||| ||||||||||||||||||||| || ||||
Db        807 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 866

Qy        852 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 911
              |  |  |||| |   |      ||||   |||| ||| | ||| ||||   ||||||  |
Db        867 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 926

Qy        912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 971
              |  | |||| ||        ||||||| ||  ||||| ||||||| |||||  |  |  | ||
Db        927 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 986

Qy        972 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
              |||||||| |||| ||  | |  | |||||||||||| || || ||| |  ||   |  ||
Db        987 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1046

Qy       1032 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1091
              | || ||||||    | | |  || |||   |||||||||||||| |||    |  || |
Db       1047 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1103

Qy       1092 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1151
               || | | | ||  | |        |||||||  ||  | || |||  | | || || ||
Db       1104 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1163

Qy       1152 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
              | | || || |   | || ||| |  |    ||| | ||| |||     |||||  || |
Db       1164 GATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1223

Qy       1212 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
              ||          | | | |   |   | |      |       | | |  |||
Db       1224 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGCTTTTCCCCGCAGGCCCGCTC 1283

Qy       1272 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331
              |  |   |    |||| |||      |     | || |  |      |  |  | |  | |  |
Db       1284 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGCCTGGGGTGTCGTGGGGGCAG 1343

Qy       1332 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1391
                |    ||    | | | || |   |||||| | | | |||||    || |||| |||
Db       1344 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1403

Qy       1392 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1451
              |||| |  | || || || ||   ||| |||||    |    ||||   ||| ||  |
Db       1404 TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGTTCT 1463

Qy       1452 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1511
               || |||||  | ||||||  |||   ||| |||||  | ||    |  ||  || | ||
Db       1464 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGGACTT 1523

Qy       1512 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1571
              || | | || ||||| |||||   ||| || ||  | |||||| | || ||  | || ||
Db       1524 CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1583

Qy       1572 GGGACTGTTTGAGGAACTGAATGAC 1596
               |     ||  | || ||||||| |
Db       1584 CGAGTGCTTCCAAGAGCTGAATGTC 1608

RESULT 10
US-08-454-439-12
; Sequence 12, Application US/08454439
; Patent No. 5591618
;  GENERAL INFORMATION:
;    APPLICANT:  Chantry, David
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Hoekstra, Merle F.
;    TITLE OF INVENTION:  A No. 5591618el G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/454,439
;      FILING DATE:  30-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/221,817
;      FILING DATE:  31-MAR-1994
;      APPLICATION NUMBER:  08/123,932
;      FILING DATE:  17 SEP 1993
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5591618and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31981
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2204 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  31..1758
US-08-454-439-12

  Query Match             25.2%;  Score 418.2;  DB 1;  Length 2204;
  Best Local Similarity   56.2%;  Pred. No. 1.1e-93;
  Matches  890;  Conservative    0;  Mismatches  683;  Indels   12;  Gaps    5;

Qy         15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74
              ||  || || ||| |  | || ||||| |     ||  |||||||| |       |   |
Db         33 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 92

Qy         75 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
                |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db         93 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 152

Qy        132 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 191
               ||||  |||||| || |  |  ||    |   |||  ||||||||||| |||| ||| |
Db        153 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACCG 212

Qy        192 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 251
              ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db        213 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 272

Qy        252 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 311
                ||||||| || |  |||    | |  ||  || ||  ||| |        || |   |
Db        273 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 332

Qy        312 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 371
               | || ||| |   |   |   | || |  |||   | | |  || |    |   |
Db        333 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 389

Qy        372 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                ||| | | |||   ||| | | |  |  || ||| ||     | | |     || |
Db        390 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 448
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Qy       432 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 491
               ||            | |  ||||||  ||   |  | | ||   | |   || |||
Db       449 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 506

Qy       492 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
              || | | |   ||||  || || | ||   || ||||||||||||     | || | |||
Db       507 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 566

Qy       552 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
              |||||| |  | ||   |||||   | | | |||| ||||| ||||||||| ||||||||
Db       567 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGTAAAGGTGGCTTTGGGGA 626

Qy       612 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
             ||| || |||  |||||||     ||| || ||||||||||||||| |||| || || ||
Db       627 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 686

Qy       672 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 731
              |||||| | ||||||      || |||   ||||| ||    || ||| | ||| ||||
Db       687 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 746

Qy       732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 791
             ||| || | |||    ||  | ||     ||||||| |||| ||||| ||||  |   ||
Db       747 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTATGAGACCAAGGACGCGCT 806

Qy       792 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 851
              ||||| ||  |||  |||||||| ||||| |||||||||||||||||||||| || ||||
Db       807 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 866

Qy       852 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 911
             |  |  |||| |   |       ||||   |||| ||| | ||| ||||   ||||||  |
Db       867 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 926

Qy       912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 971
             |  | |||| ||        ||||||| ||  ||||| |||||| |||||  |  | ||
Db       927 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 986

Qy       972 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
             |||||||| |||| ||  | |  | ||||||||||| || || ||| |  ||   |  ||
Db       987 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1046

Qy      1032 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1091
             | || ||||||    | | |  || |||   |||||||||||||| |||    |  || |
Db      1047 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1103

Qy      1092 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1151
              || | | | ||  | |        |||||||  ||  | || |||  | | || || ||
Db      1104 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1163

Qy      1152 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
             | | || || |   | || ||| |  |    ||| | |||  |||     |||||  || |
Db      1164 GATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1223

Qy      1212 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
             ||          | | | |   |   | |      |         | | |  |||
Db      1224 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGCTTTTCCCCGCAGGCCCGCTC 1283

Qy      1272 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331
             |  |   |    |||| |||      |     | || |  |      |  |  | |  |
Db      1284 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGCCTGGGGTGTCGTGGGGGCAG 1343

Qy      1332 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1391
               |    ||    | | | || |   |||||| | | | |||||    || |||| |||
Db      1344 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1403

Qy      1392 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1451
             |||| |  | || || || ||   ||| |||||    |   ||||   ||| ||  |
Db      1404 TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGTTCT 1463

Qy      1452 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1511
              || |||||  | ||||||  |||   ||| |||||  | ||    |  ||  || | ||
Db      1464 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGGACTT 1523

Qy      1512 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1571
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             || | | || ||||| |||||   ||| || ||  | |||||| | || ||  | || ||
Db      1524 CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1583

Qy      1572 GGGACTGTTTGAGGAACTGAATGAC 1596
              |     ||  | || |||||||| |
Db      1584 CGAGTGCTTCCAAGAGCTGAATGTC 1608

RESULT 11
PCT-US94-10487-12
; Sequence 12, Application PC/TUS9410487
;  GENERAL INFORMATION:
;    APPLICANT:  ICOS Corporation
;    TITLE OF INVENTION:  A Novel G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/10487
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/221,817
;      FILING DATE:  31 MAR 1994
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/123,932
;      FILING DATE:  17 SEP 1993
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Noland, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  27866/31981
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2204 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  31..1758
PCT-US94-10487-12

  Query Match             25.2%;  Score 418.2;  DB 5;  Length 2204;
  Best Local Similarity   56.2%;  Pred. No. 1.1e-93;
  Matches  890;  Conservative    0;  Mismatches  683;  Indels   12;  Gaps    5;

Qy        15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74
             ||  || || ||| |  | || ||||| |     ||  |||||||| |       |   |
Db        33 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 92

Qy        75 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
               |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db        93 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 152
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Qy        132 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 191
               ||||  ||||| || |  |  ||    |   |||  ||||||||||| |||| ||| |
Db        153 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACCG 212

Qy        192 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 251
              ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db        213 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 272

Qy        252 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 311
                ||||||| || |  |||    | |  ||  || ||  ||| |        || |   |
Db        273 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 332

Qy        312 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 371
               | || ||| |   |   |   | || |  |||   | | |  || |    |   |
Db        333 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 389

Qy        372 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                ||| | | |||   ||| | | |  |  || ||| ||     | | |     || |
Db        390 GGTCCCCCGGCAGCTGGTGACGAAC-TGCACCCAGCGGCTGGAGCAGGGTCCCTGCAAAG 448

Qy        432 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 491
                ||            | |  ||||||  ||   |  | | ||   | |   || |||
Db        449 ACCTTTTCCAGGAACTCACCCGGCTGA--CCCACGAGTACCTGAGCGTGGCCCCTTTTGC 506

Qy        492 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
               || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db        507 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 566

Qy        552 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
               |||||| |  | ||   |||||   | | | |||| ||||| |||||||| ||||||||
Db        567 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGTAAAGGTGGCTTTGGGGA 626

Qy        612 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
              ||| || |||  |||||||     ||| || |||||||||||||| ||||| || || ||
Db        627 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 686

Qy        672 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 731
               |||||| | ||||||      || |||   ||||| ||    || ||| | ||| ||||
Db        687 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 746

Qy        732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 791
              ||| || | |||    ||  | ||     ||||||| |||| ||||| ||||  |   ||
Db        747 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTGGCCTACGCCTATGAGACCAAGGACGCGCT 806

Qy        792 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 851
               ||||| ||  |||  |||||||| ||||| ||||||||||||||||||||| || ||||
Db        807 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 866

Qy        852 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 911
              |  |  |||| |   |      ||||   |||| ||| | ||| ||||   ||||||  |
Db        867 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 926

Qy        912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 971
              |  | |||| ||        ||||||| ||  ||||| ||||||| |||||  |  | ||
Db        927 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 986

Qy        972 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
              |||||||| |||| ||  | |  | ||||||||||| || || ||| |  ||    | ||
Db        987 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1046

Qy       1032 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1091
              | || ||||||    | | |  || |||   |||||||||||||| |||    |  || |
Db       1047 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1103

Qy       1092 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1151
               || | | | ||  | |        |||||||  ||  | || |||  | | || || ||
Db       1104 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1163

Qy       1152 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
              | | || || |   | || ||| |  |    ||| | ||| |||     |||||  || |
Db       1164 GATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1223

Qy       1212 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
              ||          | | | |   |   | |      |       | | |  |||
Db       1224 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGCTTTTCCCCGCAGGCCCGCTC 1283

Qy       1272 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331
              |  |   |    |||| |||      |     | || |  |      |  |  | |  |
Db       1284 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACGCCTGGGGTGTCGTGGGGGCAG 1343

Qy       1332 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1391
                |    ||    | | | || |   ||||||| | | | |||||    || |||| |||
Db       1344 TGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGGAGC 1403

Qy       1392 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1451
              |||| |  | || || || ||   ||| |||||    |   ||||   ||| ||  |
Db       1404 TGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGTTCT 1463

Qy       1452 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1511
               || |||||  | ||||||  |||   ||| |||||  | ||    |  ||  || | ||
Db       1464 GGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGGACTT 1523

Qy       1512 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1571
              || | | || ||||| |||||   ||| || ||  | |||||| | || ||  | || ||
Db       1524 CTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1583

Qy       1572 GGACTGTTTGAGGAACTGAATGAC 1596
               |     ||  | || ||||||| |
Db       1584 CGAGTGCTTCCAAGAGCTGAATGTC 1608

RESULT 12
US-08-221-817-21
; Sequence 21, Application US/08221817
; Patent No. 5532151
;  GENERAL INFORMATION:
;    APPLICANT:  Chantry, David
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Hoekstra, Merle F.
;    TITLE OF INVENTION:  A No. 5532151el G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,817
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/123,932
;      FILING DATE:  17 SEP 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5532151and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31981
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  21:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1983 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  13..1740
US-08-221-817-21

  Query Match             23.9%;  Score 395.8;  DB 1;  Length 1983;
  Best Local Similarity   55.3%;  Pred. No. 3.5e-88;
  Matches  876;  Conservative    0;  Mismatches  697;  Indels   12;  Gaps    5;

Qy           15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74
                ||  || || ||| |  | || ||||| |     ||  |||||||| |       | | |
Db           15 GGAGCTCGAGAACATCGTAGCGAACACGGGGCTACTCAAGGCCCGGGAAGGTGGTGGCGG 74

Qy           75 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
                  |  | ||||   ||    ||||    ||||| |  |  |||    | |||    |      
Db           75 GAATCGTAAAGGCAAGAGCAAGAAATGGCGCCAGATGCTGCAGTTCCCCCACATCAGCCA 134

Qy          132 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 191
                 || |  |||||||| |  |   ||   |   ||| ||||||||||||||||  ||| |
Db          135 GTGTGAAGAGCTCCGGCTCACCTTGGAACGTGACTACCACAGCCTGTGTGAGCGTCAGTC 194

Qy          192 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 251
                ||| || ||||   | ||  |||| |     || ||   |||   | |    |       |
Db          195 CATTGGGCGCCTGTTATTATGTGAGTTCTGCGCTACGAGGCCTGAGCTGACCCGCTGTAC 254

Qy          252 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 311
                  ||||||| || |  |||    | |  ||| || ||   || |          || |   |
Db          255 TGCCTTCCTGGATGGGGTGGCTGAGTATGAGGTGACCCCTGATGAGAAACGGAAGGCATG 314

Qy          312 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 371
                 | ||  |    ||||  ||   | || |  |||   | | |  || |     |   |    
Db          315 TGGGCGTC---GGCTAATGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 371

Qy          372 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                  | | | | |||   |||   | |  ||||| ||| || |   | | |     || |  
Db          372 AGTTCCCCGGCAGCTGGTGAGTAAC-TGTGCCCAGCGGCTAGAGCAGGGACCCTGCAAAG 430

Qy          432 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 491
                  ||              |  ||||||  |    |         ||| | ||  || |||  
Db          431 ACCTCTTCCAGGAGCTGACCCGGCTGACCCATGAGTACCTAAGCATGGGC--CCTTTTGG 488

Qy          492 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
                 || | | |   ||||  || || | ||   || ||||||||||||     | || | |||
Db          489 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 548

Qy          552 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
                 |||||| |  | ||   ||| |   |||  | |||| ||||| ||||||||| ||||||||
Db          549 GCCAGTGACCAAAAACACCTTTAGGCAGTACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 608

Qy          612 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
                ||| ||||||  |||||||   |  || || ||||||||||| |  || ||   | | ||
Db          609 GGTGTGTGCCTGCCAGGTGCGGACAACAGGCAAGATGTATGCGTACAAAAACTGGAAAAA 668

Qy          672 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 731
                ||| ||  | ||||||      || |||    ||| |||||   || ||| | ||| ||||
Db          669 GAAACGAATAAAGAAGCGGAAGGGGGAGGCCATGTCTCTCAACGAGAAGCAGATCCTGGA 728

Qy          732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 791
                ||| || | |||    ||  | ||     | ||||| || | ||||| ||||      ||
Db          729 GAAAGTGAACAGTAGGTTTGTAGTGATCTTAGCCTACGCATATGAGACCAAGGATGCACT 788

Qy          792 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 851
                 ||||| ||  |||   |||||||||| || |||||||||||||||||||||| || ||||
Db          789 GTGCCTGGTGCTGACATTGATGAATGGAGGCGACCTCAAGTTCCACATCTACCACATGGG 848

Qy          852 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 911
                |  |  |||| |   |      || |   | || ||  | ||| ||||   ||||||  |
Db          849 CCAGGCTGGCTTTCCCGAAGCACGTGCTGTGTTCTATGCTGCCGAGATCTGCTGTGGTCT 908

Qy          912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 971
                |  | || | ||        ||||||| ||  ||||| | ||||| |||||| | |||||
Db          909 GGAGGACTTACACCGGGAACGCATCGTGTACAGGGACCTAAAGCCAGAGAATATCCTTCT 968

Qy          972 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
                ||||||||  ||| ||    |  | || ||||||||| ||||| ||| |  |    |  ||
Db          969 GGATGACCATGGCCACATTCGAATCTCCGACCTGGGCCTGGCTGTGCATGTTCCTGAGGG 1028

Qy         1032 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1091
                | || ||||||      | |  || ||    || ||||||||||| |||    |  || |
Db         1029 CCAGACCATCAAAGGCCGTGTGGGCACTGTGGGCTACATGGCTCCAGAG---GTGGTGAA 1085

Qy         1092 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1151
                 || |   | ||  | |    |   |||||||  ||  | || |||  | | || || ||
Db         1086 GAATGAGCGCTACACATTCAGTCCTGACTGGTGGGCGCTAGGCTGCCTCCTGTACGAGAT 1145

Qy         1152 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
                | |||| ||||   | || ||| |  |    ||| | ||| |||     |||||  || |
Db         1146 GATTGCGGGACAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1205

Qy         1212 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
                ||          | | |  |  |   | | |    |        || | || ||| |     
Db         1206 GCGGCTGGTCAAGGAGGTGGCTGAGGAGTACACCGACCGCTTCTCCCCACAGGCACGCTC 1265

Qy         1272 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331
                |     ||    |||  ||       |     | ||||  |      |  |  |||    
Db         1266 ACTCTGTTCTCAGCTTCTCAACAAGGACCCTGCTGAGCGCCTGGGGTGTCGTGGAGGTGG 1325

Qy         1332 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1391
                  |   |||    | | | || |   | || || |   | || ||    || |||| |||
Db         1326 TGCCCGTGAGGTAAAGGAGCACCCCCTTTTCAAGAAACTGAATTTCAAGCGGCTGGGAGC 1385

Qy         1392 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1451
                |||  |  | ||||| || |||   || ||||||    |   ||||   ||| ||| |   
Db         1386 TGGAATGCTAGAACCACCTTTTAAACCTGACCCCCAGGCCATTTACTGCAAGGACGTGCT 1445

Qy         1452 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1511
                 || |||||  | |||||    |||   || |||||  | ||   || ||||  |  | ||
Db         1446 GGACATTGAACAGTTCTCCACAGTTAAAGGTGTGGATCTGGAGCCCACAGACCAAGACTT 1505

Qy         1512 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1571
                || |   || ||||| || |||  |||  | ||  | |||||| | || ||  | || ||
Db         1506 CTACCAGAAGTTTGCCACGGGTAGTGTGTCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1565

Qy         1572 GGGACTGTTTGAGGAACTGAATGAC 1596
                 |     ||  ||||||| |||| |
Db         1566 TGAGTGCTTCCAGGAACTAAATGTC 1590

RESULT 13
US-08-454-439-21
; Sequence 21, Application US/08454439
; Patent No. 5591618
;  GENERAL INFORMATION:
;    APPLICANT:  Chantry, David
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Hoekstra, Merle F.
;    TITLE OF INVENTION:  A No. 5591618el G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/454,439
;      FILING DATE:  30-MAY-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/221,817
;       FILING DATE:  31-MAR-1994
;       APPLICATION NUMBER:  08/123,932
;       FILING DATE:  17 SEP 1993
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  No. 5591618and, Greta E.
;       REGISTRATION NUMBER:  35,302
;       REFERENCE/DOCKET NUMBER:  31981
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312) 474-6300
;       TELEFAX:  (312) 474-0448
;       TELEX:  25-3856
;   INFORMATION FOR SEQ ID NO:  21:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1983 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  13..1740
US-08-454-439-21

  Query Match             23.9%;  Score 395.8;  DB 1;  Length 1983;
  Best Local Similarity   55.3%;  Pred. No. 3.5e-88;
  Matches  876;  Conservative    0;  Mismatches  697;  Indels   12;  Gaps    5;

Qy         15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74
              ||  || || ||| |  | || ||||| |     ||  |||||||| |       | | |
Db         15 GGAGCTCGAGAACATCGTAGCGAACACGGGGCTACTCAAGGCCCGGGAAGGTGGTGGCGG 74

Qy         75 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
                |  | ||||   ||    ||    |||| |  |  |||    | |||    |
Db         75 GAATCGTAAAGGCAAGAGCAAGAAATGGCGCCAGATGCTGCAGTTCCCCCACATCAGCCA 134

Qy        132 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 191
               || |  |||||||| |  |   ||   |   ||| |||||||||||||||||  ||| |
Db        135 GTGTGAAGAGCTCCGGCTCACCTTGGAACGTGACTACCACAGCCTGTGTGAGCGTCAGTC 194

Qy        192 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 251
              ||| || ||||   | ||  |||| |||   || ||   |||   | |   |       |
Db        195 CATTGGGCGCCTGTTATTATGTGAGTTCTGCGCTACGAGGCCTGAGCTGACCCGCTGTAC 254

Qy        252 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 311
                ||||||| || |  |||    | |  ||| || ||   || |        || |   |
Db        255 TGCCTTCCTGGATGGGGTGGCTGAGTATGAGGTGACCCCTGATGAGAAACGGAAGGCATG 314

Qy        312 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 371
               | ||  |   ||||  ||   | || |  |||   | | |  || |    |   |
Db        315 TGGGCGTC---GGCTAATGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 371

Qy        372 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                | | | | |||   |||   | |  ||||| ||| || |   | | |     || |
Db        372 AGTTCCCCGGCAGCTGGTGAGTAAC-TGTGCCCAGCGGCTAGAGCAGGGACCCTGCAAAG 430

Qy        432 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 491
                ||              |  ||||||  |    |       ||| | ||  || |||
Db        431 ACCTCTTCCAGGAGCTGACCCGGCTGACCCATGAGTACCTAAGCATGGGC--CCTTTTGG 488

Qy        492 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
               || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db        489 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 548

Qy        552 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
               |||||  |  | ||   ||| |   ||| | |||| ||||| |||||||| ||||||||
Db        549 GCCAGTGACCAAAAACACCTTTAGGCAGTACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 608

Qy        612 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
              ||| ||||||  |||||||   |  || || ||||||||||| |  || ||   | | ||
Db        609 GGTGTGTGCCTGCCAGGTGCGGACAACAGGCAAGATGTATGCGTACAAAAACTGGAAAAA 668

Qy        672 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 731
              ||| ||  | ||||||      || |||   ||| |||||   || ||| | ||| ||||
Db        669 GAAACGAATAAAGAAGCGGAAGGGGGAGGCCATGTCTCTCAACGAGAAGCAGATCCTGGA 728

Qy        732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 791
              ||| || | |||    ||  | ||     | ||||| || | ||||| ||||      ||
Db        729 GAAAGTGAACAGTAGGTTTGTAGTGATCTTAGCCTACGCATATGAGACCAAGGATGCACT 788

Qy        792 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 851
               ||||| ||  |||   |||||||||| || ||||||||||||||||||||| || ||||
Db        789 GTGCCTGGTGCTGACATTGATGAATGGAGGCGACCTCAAGTTCCACATCTACCACATGGG 848

Qy        852 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 911
              |  |  |||| |   |      || |   | || ||  | ||| ||||   ||||||  |
Db        849 CCAGGCTGGCTTTCCCGAAGCACGTGCTGTGTTCTATGCTGCCGAGATCTGCTGTGGTCT 908

Qy        912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 971
              |  | || | ||        ||||||| ||  ||||| | ||||| |||||| | |||||
Db        909 GGAGGACTTACACCGGGAACGCATCGTGTACAGGGACCTAAAGCCAGAGAATATCCTTCT 968

Qy        972 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
              ||||||||  ||| ||    |  | || ||||||||| ||||| ||| |  |    |  ||
Db        969 GGATGACCATGGCCACATTCGAATCTCCGACCTGGGCCTGGCTGTGCATGTTCCTGAGGG 1028

Qy       1032 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1091
              | || ||||||      | |  || ||    || ||||||||||| |||    |  || |
Db       1029 CCAGACCATCAAAGGCCGTGTGGGCACTGTGGGCTACATGGCTCCAGAG---GTGGTGAA 1085

Qy       1092 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1151
               || |   | ||  | |    |   |||||||  ||  | || |||  | | || || ||
Db       1086 GAATGAGCGCTACACATTCAGTCCTGACTGGTGGGCGCTAGGCTGCCTCCTGTACGAGAT 1145

Qy       1152 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
              | |||| ||||   | || ||| |  |    ||| | ||| |||     |||||  || |
Db       1146 GATTGCGGGACAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1205

Qy       1212 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
              ||          | | |  |  |   | | |    |      || | || ||| |
Db       1206 GCGGCTGGTCAAGGAGGTGGCTGAGGAGTACACCGACCGCTTCTCCCCACAGGCACGCTC 1265

Qy       1272 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331
              |     ||    |||  ||       |     | ||||  |      |  |  |||
Db       1266 ACTCTGTTCTCAGCTTCTCAACAAGGACCCTGCTGAGCGCCTGGGGTGTCGTGGAGGTGG 1325

Qy       1332 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1391
                |   |||    | | | || |   | || || |   | || ||    || |||| |||
Db       1326 TGCCCGTGAGGTAAAGGAGCACCCCCTTTTCAAGAAACTGAATTTCAAGCGGCTGGGAGC 1385

Qy       1392 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1451
              |||  |  | ||||| || |||   || |||||    |   ||||   ||| ||| |
Db       1386 TGGAATGCTAGAACCACCTTTTAAACCTGACCCCCAGGCCATTTACTGCAAGGACGTGCT 1445

Qy       1452 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1511
               || |||||  | |||||    |||   || |||||  | ||   || |||  |  | ||
Db       1446 GGACATTGAACAGTTCTCCACAGTTAAAGGTGTGGATCTGGAGCCCACAGACCAAGACTT 1505

Qy       1512 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1571
              || | | || ||||| || |||  |||  | ||  | |||||| | || ||  | || ||
Db       1506 CTACCAGAAGTTTGCCACGGGTAGTGTGTCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1565

Qy       1572 GGGACTGTTTGAGGAACTGAATGAC 1596
               |     ||  ||||||| |||| |
Db       1566 TGAGTGCTTCCAGGAACTAAATGTC 1590

RESULT 14
PCT-US94-10487-21
; Sequence 21, Application PC/TUS9410487
;  GENERAL INFORMATION:
;    APPLICANT:  ICOS Corporation
;    TITLE OF INVENTION:  A Novel G Protein-Coupled Receptor
;     TITLE OF INVENTION:  Kinase GRK6
;     NUMBER OF SEQUENCES:  24
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;       ADDRESSEE:  Borun
;       STREET:  6300 Sears Tower, 233 South Wacker Drive
;       CITY:  Chicago
;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60606
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/10487
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/221,817
;       FILING DATE:  31 MAR 1994
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/123,932
;       FILING DATE:  17 SEP 1993
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Noland, Greta E.
;       REGISTRATION NUMBER:  35,302
;       REFERENCE/DOCKET NUMBER:  27866/31981
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312) 474-6300
;       TELEFAX:  (312) 474-0448
;       TELEX:  25-3856
;   INFORMATION FOR SEQ ID NO:  21:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1983 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  13..1740
PCT-US94-10487-21

  Query Match             23.9%;  Score 395.8;  DB 5;  Length 1983;
  Best Local Similarity   55.3%;  Pred. No. 3.5e-88;
  Matches  876;  Conservative    0;  Mismatches  697;  Indels   12;  Gaps    5;

Qy          15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74
               ||  || || ||| |  | || ||||| |     ||  |||||||| |       | | |
Db          15 GGAGCTCGAGAACATCGTAGCGAACACGGGGCTACTCAAGGCCCGGGAAGGTGGTGGCGG 74

Qy          75 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
                 |  | ||||   ||    ||||    ||||  |  |  |||    | |||    |
Db          75 GAATCGTAAAGGCAAGAGCAAGAAATGGCGCCAGATGCTGCAGTTCCCCCACATCAGCCA 134

Qy         132 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 191
                || |  |||||||| |  |   ||   |   ||| ||||||||||||||||||  ||| |
Db         135 GTGTGAAGAGCTCCGGCTCACCTTGGAACGTGACTACCACAGCCTGTGTGAGCGTCAGTC 194

Qy         192 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 251
               ||| || ||||   | ||  |||| |||   || ||   |||   | |   |       |
Db         195 CATTGGGCGCCTGTTATTATGTGAGTTCTGCGCTACGAGGCCTGAGCTGACCCGCTGTAC 254

Qy         252 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 311
                 ||||||| || |  |||    | |  ||| || ||   || |         || |   |
Db         255 TGCCTTCCTGGATGGGGTGGCTGAGTATGAGGTGACCCCTGATGAGAAACGGAAGGCATG 314

Qy         312 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 371
                | ||  |   ||||  ||   | || |  |||   | | |  || |     |   |
Db         315 TGGGCGTC---GGCTAATGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 371

Qy         372 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                 | | | | |||   |||   | |  ||||| ||| || |   | | |     || |
Db         372 AGTTCCCCGGCAGCTGGTGAGTAAC-TGTGCCCAGCGGCTAGAGCAGGGACCCTGCAAAG 430

Qy         432 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 491
                 ||              |  ||||||  |    |       ||| | ||  || |||
Db         431 ACCTCTTCCAGGAGCTGACCCGGCTGACCCATGAGTACCTAAGCATGGGC--CCTTTTGG 488

Qy         492 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
                || | | |   ||||  || || | ||  || ||||||||||     | || | |||
Db         489 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 548

Qy         552 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
                |||||| |  | ||   ||| |   ||| | |||| ||||| ||||||||| ||||||||
Db         549 GCCAGTGACCAAAAACACCTTTAGGCAGTACCGAGTCCTGGGCAAAGGTGGCTTTGGGGA 608

Qy         612 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
               ||| ||||||  |||||||   |  || || ||||||||||| |  || ||   | | ||
Db         609 GGTGTGTGCCTGCCAGGTGCGGACAACAGGCAAGATGTATGCGTACAAAAACTGGAAAAA 668

Qy         672 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 731
               ||| ||  | ||||||      || |||   ||| |||||   || |||  | ||| ||||
Db         669 GAAACGAATAAAGAAGCGGAAGGGGGAGGCCATGTCTCTCAACGAGAAGCAGATCCTGGA 728

Qy         732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 791
               ||| || | |||    ||  | ||     | ||||| || | ||||| ||||      ||
Db         729 GAAAGTGAACAGTAGGTTTGTAGTGATCTTAGCCTACGCATATGAGACCAAGGATGCACT 788

Qy         792 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 851
                ||||| ||  |||   |||||||||| || ||||||||||||||||||||||| || ||||
Db         789 GTGCCTGGTGCTGACATTGATGAATGGAGGCGACCTCAAGTTCCACATCTACCACATGGG 848

Qy         852 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 911
               |  |  |||| |   |      || |   | || ||  | ||| ||||   ||||||  |
Db         849 CCAGGCTGGCTTTCCCGAAGCACGTGCTGTGTTCTATGCTGCCGAGATCTGCTGTGGTCT 908

Qy         912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 971
               |  | || | ||        ||||||| ||  ||||| | ||||| |||||| | |||||
Db         909 GGAGGACTTACACCGGGAACGCATCGTGTACAGGGACCTAAAGCCAGAGAATATCCTTCT 968

Qy         972 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
               ||||||||  ||| ||    |  | || |||||||| |||| ||| |  |    |  ||
Db         969 GGATGACCATGGCCACATTCGAATCTCCGACCTGGGCCTGGCTGTGCATGTTCCTGAGGG 1028

Qy        1032 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1091
               | || ||||||      | |  || ||    || |||||||||||| |||    |  || |
Db        1029 CCAGACCATCAAAGGCCGTGTGGGCACTGTGGGCTACATGGCTCCAGAG---GTGGTGAA 1085

Qy        1092 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1151
                || |   | ||  | |    |   |||||||  ||  | || |||  | | || || ||
Db        1086 GAATGAGCGCTACACATTCAGTCCTGACTGGTGGGCGCTAGGCTGCCTCCTGTACGAGAT 1145

Qy        1152 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
               | |||| ||||   | || ||| |  |    ||| | ||| |||     |||||  || |
Db        1146 GATTGCGGGACAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1205

Qy        1212 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
               ||          | | |  |  |   | | |    |      || | || ||| |
Db        1206 GCGGCTGGTCAAGGAGGTGGCTGAGGAGTACACCGACCGCTTCTCCCCACAGGCACGCTC 1265

Qy        1272 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331
               |     ||    |||  ||       |     | ||||  |      |  |  |||
Db        1266 ACTCTGTTCTCAGCTTCTCAACAAGGACCCTGCTGAGCGCCTGGGGTGTCGTGGAGGTGG 1325

Qy        1332 GTCTGATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGAAGC 1391
                 |   |||    | | | || |   | || || |   | || ||    || |||| |||
Db        1326 TGCCCGTGAGGTAAAGGAGCACCCCCTTTTCAAGAAACTGAATTTCAAGCGGCTGGGAGC 1385

Qy        1392 TGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACATCGC 1451
               |||  |  | ||||| || |||   || ||||||    |   ||||   ||| ||| |
Db        1386 TGGAATGCTAGAACCACCTTTTAAACCTGACCCCCAGGCCATTTACTGCAAGGACGTGCT 1445
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```
Qy       1452 TGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCAGTT 1511
               || |||||  | |||||    |||   || |||||  | ||   || |||  |  | ||
Db       1446 GGACATTGAACAGTTCTCCACAGTTAAAGGTGTGGATCTGGAGCCCACAGACCAAGACTT 1505

Qy       1512 CTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGAAAC 1571
              || | | || ||||| || |||  |||  | ||  | |||||| | || ||  | || ||
Db       1506 CTACCAGAAGTTTGCCACGGGTAGTGTGTCCATCCCCTGGCAGAACGAGATGGTGGAGAC 1565

Qy       1572 GGGACTGTTTGAGGAACTGAATGAC 1596
               |     ||  ||||||| |||| |
Db       1566 TGAGTGCTTCCAGGAACTAAATGTC 1590

RESULT 15
US-08-221-817-10
; Sequence 10, Application US/08221817
; Patent No. 5532151
;  GENERAL INFORMATION:
;    APPLICANT:  Chantry, David
;    APPLICANT:  Gray, Patrick W.
;    APPLICANT:  Hoekstra, Merle F.
;    TITLE OF INVENTION:  A No. 5532151el G Protein-Coupled Receptor
;    TITLE OF INVENTION:  Kinase GRK6
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/221,817
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/123,932
;      FILING DATE:  17 SEP 1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  No. 5532151and, Greta E.
;      REGISTRATION NUMBER:  35,302
;      REFERENCE/DOCKET NUMBER:  31981
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2206 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  31..1926
US-08-221-817-10

  Query Match             23.5%;  Score 389.4;  DB 1;  Length 2206;
  Best Local Similarity   55.3%;  Pred. No. 1.4e-86;
  Matches  866;  Conservative    0;  Mismatches  681;  Indels   18;  Gaps    5;

Qy         15 GGCCCTGGACAACCTGATCGCCAACACCGCCTACCTGCAGGCCCGGAAGCCCTCGGACTG 74
              ||  || || ||| |  | || ||||| |     ||  |||||||| |       |   |
Db         33 GGAGCTCGAGAACATCGTAGCGAACACGGTGCTACTCAAGGCCCGGGAAGGTGGCGGTGG 92

Qy         75 CGACAGCAAAG---AGCTGCAGCGGCGGCGGCGTAGCCTGGCCCTGCCCGGGCTGCAGGG 131
                |  ||||||   |     ||    ||||||  |  ||     | ||     |
Db         93 AAATCGCAAAGGCAAAAGCAAGAAATGGCGGCAGATGCTCCAGTTCCCTCACATCAGCCA 152

Qy        132 CTGCGCGGAGCTCCGCCAGAAGCTGTCCCTGAACTTCCACAGCCTGTGTGAGCAGCAGCC 191
               ||||  ||||| || |  |  ||    |   |||  ||||||||||| |||| ||| |
Db        153 GTGCGAAGAGCTGCGGCTCAGCCTCGAGCGTGACTATCACAGCCTGTGCGAGCGGCACCG 212

Qy        192 CATCGGTCGCCGCCTCTTCCGTGACTTCCTAGCCACAGTGCCCACGTTCCGCAAGGCGGC 251
              ||| || ||||  || ||||| || |||   |||||   |||   | |  ||      |
Db        213 CATTGGGCGCCTGCTGTTCCGAGAGTTCTGTGCCACGAGGCCGGAGCTGAGCCGCTGCGT 272

Qy        252 AACCTTCCTAGAGGACGTGCAGAACTGGGAGCTGGCCGAGGAGGGACCCACCAAAGACAG 311
                ||||||| || |  |||    | |  ||  || ||  ||| |        || |   |
Db        273 CGCCTTCCTGGATGGGGTGGCCGAGTATGAAGTGACCCCGGATGACAAGCGGAAGGCATG 332

Qy        312 CGCGCTGCAGGGGCTGGTGGCCACTTGTGCGAGTGCCCCTGCCCCGGGGAACCCGCAACC 371
               | || ||| |   |   |   | || |  |||   | | |  || |     |   |
Db        333 TGGGCGGCACG---TAACGCAGAATTTTCTGAGCCACACGGGTCCTGACCTCATCCCTGA 389

Qy        372 CTTCCTCAGCCAGGCCGTGGCCACCAAGTGCCAAGCAGCCACCACTGAGGAAGAGCGAGT 431
                ||| | | |||   ||| |   |     |||             ||| | |  |  |
Db        390 GGTCCCCCGGCAGCTGGTGACGGACTGCACCCAGCG------GCTGGAGCAGGGTCCTGC 443

Qy        432 GGCTGCAGTGACGCTGCGCAAGGCTGAGGCCATGGCTTTCTTGCAAGAGCAGCCCTTTAA 491
                   |  |  |   |  | |  | |  | |       |     |       ||||||
Db        444 AAAGACCTTTTCCAGGAACTACCCGGCTGACCCACGAGTACCTGAGCGTGGCCCCTTTGC 503

Qy        492 GGATTTCGTGACCAGCGCCTTCTACGACAAGTTTCTGCAGTGGAAACTCTTCGAGATGCA 551
               || | | |   ||||  || || | ||   || |||||||||||     | || | |||
Db        504 CGACTACCTCGACAGCATCTACTTCAACCGTTTCCTGCAGTGGAAGTGGCTGGAAAGGCA 563

Qy        552 ACCAGTGTCAGACAAGTACTTCACTGAGTTCAGAGTGCTGGGGAAAGGTGGTTTTGGGGA 611
               |||||| |  | ||   |||||   | | | |||| ||||| |||||||| ||||||||
Db        564 GCCAGTGACCAAAAACACCTTCAGGCAATACCGAGTCCTGGGTAAAGGTGGCTTTGGGGA 623

Qy        612 GGTATGTGCCGTCCAGGTGAAAAACACTGGGAAGATGTATGCCTGTAAGAAACTGGACAA 671
              ||| || |||  |||||||     ||| || ||||||||||||||| ||||| || || ||
Db        624 GGTGTGCGCCTGCCAGGTGCGGGCCACAGGTAAGATGTATGCCTGCAAGAAGCTAGAGAA 683

Qy        672 GAAGCGGCTGAAGAAGAAAGGTGGCGAGAAGATGGCTCTCTTGGAAAAGGAAATCTTGGA 731
               |||||| | ||||||      || |||   ||||| ||    || |||  | ||| ||||
Db        684 AAAGCGGATCAAGAAGCGGAAAGGGGAGGCCATGGCGCTGAACGAGAAGCAGATCCTGGA 743

Qy        732 GAAGGTCAGCAGCCCTTTCATTGTCTCTCTGGCCTATGCCTTTGAGAGCAAGACCCATCT 791
              ||| || | |||    ||  | ||     | | ||| ||||| ||||| ||||  |   ||
Db        744 GAAAGTGAACAGTAGGTTTGTAGTGAGCTTCGGCTACGCCTATGAGACCAAGGACGCGCT 803

Qy        792 CTGCCTTGTCATGAGCCTGATGAATGGGGGAGACCTCAAGTTCCACATCTACAACGTGGG 851
               ||||| ||  |||  ||||||||| ||||| |||||||||||||||||||||| || ||||
Db        804 GTGCCTGGTGCTGACACTGATGAACGGGGGCGACCTCAAGTTCCACATCTACCACATGGG 863

Qy        852 CACGCGTGGCCTGGACATGAGCCGGGTGATCTTTTACTCGGCCCAGATAGCCTGTGGGAT 911
              |  |  |||| |   |       ||||   |||| ||| | ||| ||||    ||||||  |
Db        864 CCAGGCTGGCTTCCCCGAAGCGCGGGCCGTCTTCTACGCCGCCGAGATCTGCTGTGGCCT 923

Qy        912 GCTGCACCTCCATGAACTCGGCATCGTCTATCGGGACATGAAGCCTGAGAATGTGCTTCT 971
              |  | |||| ||        ||||||| ||  ||||| ||||||| |||||  |  |  | ||
Db        924 GGAGGACCTGCACCGGGAGCGCATCGTGTACAGGGACCTGAAGCCCGAGAACATCTTGCT 983

Qy        972 GGATGACCTCGGCAACTGCAGGTTATCTGACCTGGGGCTGGCCGTGGAGATGAAGGGTGG 1031
              |||||||| |||| ||  | |  | |||||||||||| || || ||| |  ||   |  ||
Db        984 GGATGACCACGGCCACATCCGCATCTCTGACCTGGGACTAGCTGTGCATGTGCCCGAGGG 1043

Qy       1032 CAAGCCCATCACCCAGAGGGCTGGAACCAATGGTTACATGGCTCCTGAGATCCTAATGGA 1091
              | || ||||||    | | |  || |||   |||||||||||||| |||    |  || |
Db       1044 CCAGACCATCAAAGGGCGTGTGGGCACCGTGGGTTACATGGCTCCGGAG---GTGGTGAA 1100

Qy       1092 AAAGGTAAGTTATTCCTATCCTGTGGACTGGTTTGCCATGGGATGCAGCATTTATGAAAT 1151
               || | | | ||  | |        |||||||  ||  | || |||  | | || || ||
Db       1101 GAATGAACGGTACACGTTCAGCCCTGACTGGTGGGCGCTCGGCTGCCTCCTGTACGAGAT 1160

Qy       1152 GGTTGCTGGACGAACACCATTCAAAGATTACAAGGAAAAGGTCAGTAAAGAGGATCTGAA 1211
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                 | | || || |   | || ||| |  |    ||| | ||| |||     |||||  || |
Db          1161 GATCGCAGGCCAGTCGCCCTTCCAGCAGAGGAAGAAGAAGATCAAGCGGGAGGAGGTGGA 1220

Qy          1212 GCAAAGAACTCTGCAAGACGAGGTCAAATTCCAGCATGATAACTTCACAGAGGAAGCAAA 1271
                 ||          | | | |   |   | |      |       | | |  |||
Db          1221 GCGGCTGGTGAAGGAGGTCCCCGAGGAGTATTCCGAGCGCTTTTCCCCGCAGGCCCGCTC 1280

Qy          1272 AGATATTTGCAGGCTCTTCTTGGCTAAGAAACCAGAGCAACGCTTAGGAAGCAGAGAAAA 1331
                 |  |   |    |||| |||      |     | || |    | | ||  |  | |
Db          1281 ACTTTGCTCACAGCTCCTCTGCAAGGACCCTGCCGAACCGACCCTGGGGTGTCGTGGGGG 1340

Qy          1332 GTCTG---ATGATCCCAGGAAACATCATTTCTTTAAAACGATCAACTTTCCTCGCCTGGA 1388
                    ||     ||    | | | || |   ||||||| | | | |||||    || ||||
Db          1341 CAGTGCCCGCGAGGTGAAGGAGCACCCCCTCTTTAAGAAGCTGAACTTCAAGCGGCTGGG 1400

Qy          1389 AGCTGGCCTAATTGAACCCCCATTTGTGCCAGACCCTTCAGTGGTTTATGCCAAAGACAT 1448
                 ||||||| |  | || || || ||   |||| |||||    |   ||||   ||| ||  |
Db          1401 AGCTGGCATGCTGGAGCCGCCGTTCAAGCCTGACCCCCAGGCCATTTACTGCAAGGATGT 1460

Qy          1449 CGCTGAAATTGATGATTTCTCTGAGGTTCGGGGGGTGGAATTTGATGACAAAGATAAGCA 1508
                     || |||||  | ||||||  |||   ||| |||||  | ||    |  ||  || |
Db          1461 TCTGGACATTGAACAGTTCTCTACGGTCAAGGGCGTGGAGCTGGAGCCTACCGACCAGGA 1520

Qy          1509 GTTCTTCAAAAACTTTGCGACAGGTGCTGTTCCTATAGCATGGCAGGAAGAAATTATAGA 1568
                  |||| | | || ||||| |||||   ||| || ||  | |||||| | || ||  | ||
Db          1521 CTTCTACCAGAAGTTTGCCACAGGCAGTGTGCCCATCCCCTGGCAGAACGAGATGGTGGA 1580

Qy          1569 AACGG 1573
                  || |
Db          1581 GACCG 1585

Search completed: August 13, 2004, 18:45:37
Job time : 91.4555 secs
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